

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GGGCGGGCGG GCGCGGATTI TCTGTGCTT TGATTGTGCG TGGGGATAAC GCGCGTGATG	50
GTGTAAACCG CGGATGGGCG GGGGCTGGCG GGGCTGGCGG CCGCGGCGGG GCGCGCGGCG	120
TGATCAGGCT GCTGGGCGCG CAAGGCGCGG GCGGGGCGGG CGGACCGGCG GCGCGCGGCG	180
GTGTGGGCGG TGACGGGCGG GCGGCGGCGG CCGGCAACCA GCGCTTCAAC GCAGGTGCGG	240
GCGGCGGCGG CGGCGTGATG AGCTGTCTGG GCGGCCAAGG CCGCGGCGGG GCGGCGGCGG	300
CGGCGGCGGCG GCGCGGTGTT GCGCGTGAC	329

(2) INFORMATION FOR SEQ ID NO:164:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GCACACGCTG CAACGCGCGG ACCGACACGA CGTGGGGAT GCGCGGAGGT AACTGTGGTG	60
CGCGCGGCGT GATCGGCAAC	80

(2) INFORMATION FOR SEQ ID NO:165:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GGGCTGTGTC GCACCTCACG GCGCGGATTC GCGGACGTTG GCGCGGCAAT ATCCAGCTCA	60
AGGCTTACTA CTTACGCTCG GAGGACCGCC GCATCAAGGT GCGGGTCAGC GCGCAAGGAA	120
TCAAGGTGAT CGACCGCGAG GCGGATCGAG GCGGTGCTCG TGCGGCTCGG GCAGGATCGG	180
CGCGGCGCGA GTTCGCGCGC CAAGCGGGCT CATGCTCGCG AACGCGCGCG ATCTGTGTGAG	240
CACAAGTGAT GCGCGCGGAG GAGATTGTTC CAATTGTCAA GCGGTGTTGCG ACCGAGGGGA	300
CGGTTATAC GTATGTCAAC CTATGTCACT GCGAAGAAC GGCATAACGA TCCCGTGATC	360
CGCGGACAGC CCACAGTGTC AAGACGTTTA CA	392

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 535 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACCGGCGCCA CGGCGCGCAC CGGTTTCGCC GTTGGCGCCG GCGGGGCCCC GGGGACAGGGC	60
GGTATCAGCG GTGCGCGCCG CACCAACCGC TGTGTTGGCG CTGGCGGCAC GGGCGACAA	120
GGCGGGCCCG GGGCGCTCGG CGGGGCGCGC GCCGATAACC CCACCGGCAT CGGCGGCCCC	180
GGCGGCACCG GGGGCACCGG CGGAGCGCCC GGAGCCCGCG GGGCGGCTCG CGCCATCGGT	240
ACCGGCGCCA CGGCGCGCCG GTTGGGCAGC GTCGGTAACC CCGGATCCCG CGGTACCGGC	300
GGTACCGGTG GTGTCTGCTG TGCTGGTGGT GCAGGTGCGG CTGGCGCGCG TGCGACGACG	360
GCTACCGGTG GCGCGCGGTT CGCGGGCGGC GCGGCGGAG AAGCGCGACC GGGCGGCAAC	420
AGCGGTGTGG GGGGCACCAA CGGCTCCGGC GCGCGCGCGG GTCCAGGCGG CAGGGCGCGC	480
ACCGAGGCTG CGGCGGGTGC CGGCGCGGAC AACCCGACCG GTGCTGTTT CGCGG	535

(i) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 490 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CCGACGTCGC CGGGCGGATA CGGGGCTCAC CCACTACTAC ATCATCGGCA CCGAGATCG	60
GCGCGTCTTG CAACCTGCTG GGGCGGTGCC GTTCATCGGA GATCGGCTGG CCGACGCTAT	120
CGGCGCGAAC CTGAAGGTGA TGCTCAACTT GGGCTACGGC GACCGCAACT ACCGCTACTC	180
GACGAGCTAC GCGGATGTGC GAACGCGGTT GGGGCTGTGG CGGAACGTGC CGGCTCAGGT	240
GATGCGCGAT GCGCTGGCGG CGGGAACACA AGAAGGCATC CTTGACTTCA CGGCGACCT	300
GCAGGCGCTG TGCGCGCAAC CGCTCAGGCT CCGGCAGATC CAGCTGCGGC AACCGCGGA	360
TCTGTGGGCC GGGGTGGCGG CGGCACCGAC GCGGCGCGAG GTGGTGAACA CGCTCGCCAG	420
GATCATCTCA ACCAACTAGG CGTCTCTGCT GCGGACCGTG GACATCGGCC TGCGCTGGTG	480
ACCACCGTGC CGCTGTACAC CACCCAACTG TTGTCAGGC AACTCGCTGC GGGCAATCTG	540

ATCAACGCGA TCGGCTATCC GCTGGCGGCC ACCGTAGGTT TAGGCACGAT CGATACGCGG	600
CGGCGTGGAA TTGCTCAGCC TCTTCGCGGC GGCCTCGGAC ACCGTTGGAA ACATCGAGGG	660
GTCGTCACC TAACGGATTC CCGACGGCAT	690

## (2) INFORMATION FOR SEQ ID NO:168:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (X1) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACGCTGACGG CGGTACTGCG GCGCGCCACG GCGGCACCG CGGGAATCCC GGTGGCTCT	60
TGGGCACAGC CGGGGCTGCG GGCACGCTG GCGCCGCGCA CACGGTACT GCAGGTGGCG	120
GCTCTGGGCG CACCGCGCGC GACGGCGGGA CCGCGCGCGG TGGCGGCTG TTAATGGGCG	180
CGGCGCGCGG CGGGCACGGT GCGACTGGCG GCGCGCGCGG TCGCGGTGTC GACGGTGGCG	240
GCGCGCGCGG GCGCGCGCGG GCGCGCGCGA ACGCGCGCGC CGGGGGTCAA GCGCGCGTGC	300
TGTTGCGGCG CGGCGCGACT GCGCGGAGCG GCGGCTACGG CGGCGATGCG GGTGGCGCGG	360
GTGACGGCTT CGACGGCAGC ATGCGCGCGC TGGGTGGTAC CGGTGGC	407

## (2) INFORMATION FOR SEQ ID NO:169:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (X1) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GATCGTCAAG CGCATCGCCC TCGCGCGCAA GCGATTCCGC GGTCTCAGCG AAGAACATCG	60
TGCACGCGCG GCGCGCGACC AGCCCGCTGC GCTCGCGCGC GTCGAACGCC TCCAGCAGCG	120
ACAGCCAGTC GTTGGCGGCG TCGAGCGGGA ACAGCTCGGT GTCAAGGCTG TAGATGGCGG	180
GGATGCGCGC CTCGCGCAAC GCATTCCGCG ACGCGCGCGC GTCTTTGTGA TGCTCGAGCA	240
TCACCGCGAT GTGTGCGGCG ACCACGCGGC GCGCGCGGAA GGTGCGCGCG GTGGCTAGTA	300
GCGCGCGGAC GTGCGCGGCG AGGTGCTCGG GATGTGCGG GCGCAGCGCT CCGCGCGGAC	360
GCGCGAAGAA GCGCGCGTCA CCGAGCTGGG TCGCGCTGCG ATATCGCTTG CCGTCTCTGG	420
CGATATTGGA CCGCGATGCC CCGACTCGCT ACAGCGCGCG CAGCACCG	468

## (2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GGTGTAAAC	CGCGCCAGGG	TGGCATCGGC	GGCCCGCGCG	AGAGAGGGCG	CGACCGCGCC	60
CGCCCAATG	CTAACGCGCG	AAACGGCGAG	AACGCGGTA	CGGTGTGTA	CGGTGGCGAC	120
GGCGCGCGCG	CGCGCAATG	CGCGCGCGCG	GGCAACGCG	AGCGCGCGCG	GTACACCGAC	180
GGCGCGCGCG	CGACCGCGCG	CGACCGCGCG	AACCGCGCG			219

## (2) INFORMATION FOR SEQ ID NO:171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TAGCTCGCGC	GAGGCGCGCA	AGGCGCGCGA	CGGTGCGCAC	GGCGGTGACG	GGCTCGCGCG	60
CTACAGTTCC	GTACCTCAAG	CGCGCGCGCG	CGGTGCGCGC	GGCGCGCGCG	GGCGCGCGCG	120
CAGCGCGCTT	TTGCGCGCGA	AGGCGCGCTT	CGCGCGCGAC	GGCGGTGAGG	GGCGCGCGCA	180
CGCGCGCGGT	ACGCTCGCGA	CGGTGCGCGG	TGCGCGCGCG	AACGCGCGTG	TGCGCGCGCG	240
GGCGCGCGAC	GGCTCTTTG	CGGTGCGCGG	CGCGCGCGCG	GGCTCTTTG	GGCGCGCGCG	300
CAATGCGCGC	GGCTCGCGCG	CGCGCGCGCG	CGCGCTTTGG	GGCGCGCGCG	GTGCGCGCGG	360
CAACGCGCGG	GCTGCTGCGC	AATCGCGCGT	GACCATGCGC	AGCGCGCGCA	AGTTGCGCTG	420
CATCGCATCA	GGCGCGTACT	GGCGCGCAAC	CTGCGACAT	CACCGCGAGT	AGCGCGCGCG	480
ATTCTCTGAT	CAGC					494

## (2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## [xi] SEQUENCE DESCRIPTION: SEQ ID NO:172:

GGGCGGGTGG TGCCGCGGGC CAGCTCTTCA GCGCGGAGG GCGCGGGGT GCCGTTGGGG	60
TTGCGGCGAC CGGCGGCGAG GGTGGGGCTG GCGGTGCGGG AGCGGCGGCG GCCACGCGCC	120
CGCGGAGCAG AGGTCTAACC GGTGGTACCG GGTTCGCTGG CGGGGCGGGC GGCCTCGGGG	180
GCCAGAGCGG CAACGCCATT GCGGCGGCGA TCAACGGCTC	220

## [3] INFORMATION FOR SEQ ID NO:173:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## [xi] SEQUENCE DESCRIPTION: SEQ ID NO:173:

ATGCGGCGCA CGGGGGCGCC GCGGTGCTG GCGGGGCGCG CCACTACAAT TTCCAACGGC	60
GGGCAGGGTG GTGCGCGCGG CCAAGCGGCG CAAGCGGCGC TGCGCGGGCG AAGCACCAGC	120
TGATCGGGCT AGCGGCGCGC GGGAAAGCGG ATCCAACAGG CGACGATGC GCCTTCCTTG	180
CGCGCTTGA CAAGGCGGCG ATCACTTACG CTGACCGAGG CCACGCCATA ACGGCGGCGA	240
AGGGGATGTT TGCGCTGTGT GCTAACGCGG TAACAGGTCT ACAGCTGGTC GCGGACCTGC	300
GCGACTACAA TTCGCGGCTG ACCATGGACA GCGGCGGCAA GTTGGCTGCC ATGCGATCAG	360
GCGGCTACTG CCGCGAAGAC CTGGACAA	388

## [2] INFORMATION FOR SEQ ID NO:174:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## [xi] SEQUENCE DESCRIPTION: SEQ ID NO:174:

GCAAGGCGCG CACCGCGGCG GCGGCGATGA ACAGGCTCGA GCGGTGCTA GCGGCGGCAAG	60
ACCGGCGGCGA AGCGGCGACC GCGGCGACCG GCGGCAACGC CGGCGCGGCG GGCACGAGT	120
TCACCCGAAG CCGCGAAGCG AACCGCGGCA ACGGCGGTGA CGGCGGGCTT GCGGCGCAAG	180
GCGGAAACCG CGGAAACCGC GCAGACAACA CCACCAAGCG CCGCGCGGCG ACCACAGGCG	240
GTGACGCGCG GCGCGCGGCG GCGGCGGAA CCGGCGGAAC CCGGCGAGCC GCGGCGACCG	300
GCAACCGGCG CCAACAAGCG AACGGCGGCG ACGGCGGCGC CCGGCGGAAA GCGGCGACCG	360

GGGGGACGGG TGCATCTCA GGCAGCAGCG GTGGTCCCG

400

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 538 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGACACGGCG GCAACGGCGG CATCGCGCGC ATTGGGCGGC AACGGCGTTC CGGGACGGGC	60
AGCGGCAACG GCGGCCAAGC GCGGCACCGG CGGCACCGGC GCGAACCGCG GCATGGCGCG	120
CAACAGCGCG ACTCGCAGG GCGACGCGCG TCGCGCGCGG AACGCGCGCG CGCGCGGCAC	180
GGCGCGCACC GCGCGCGCAG CGCGCGCTCAG CGGTACTGCG GGCACCGCGG GCAAGCGTGG	240
CACCGCGCGT GACGCGCGTA ACGCGCGCAA CGGAGCGAGT AACACCGCAA ACATGACTGC	300
GCAGCGCGCG GGTGACGGTG GCAACGCGCG CGACGGTGGC TTCGGCGCGC GCGCGCGCGC	360
CGCGCGCGCG GCGTTCAGCG CTGGCGCGAA CGGCACCGCG GCGCAAGCGG GCGCGCGCGG	420
CGATGGCGCG AACGCGCGCA TCGCGCGCCA CGCGCCACTC ACTGACGACC CGCGCGCGCA	480
CGGGGCGCAG GCGGCCAAGC GCGGCACCGG CGGCACCGCG GCGCGCGCGCA TCGGCAGC	538

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 219 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GGCGCGGTGG TCGCGCGCGC CAGCTCTTCA TCGCGCGAGC CGCGCGCGGT GCGCTTGGGG	60
TTGGCGCGCA GCGCGCGCAG GTTGGCGGTC GCGGTGCGCG AGCGCGCGCG GCGGACGCGC	120
CGCGCACGAC AGCTCTAACC GTGTGTACCG GTTTCGCTGG CGCGCGCGCG GCGGTGCGCG	180
GCGACGCGCG CAACGCGATT GCGCGCGGCA TCAAGCGGTC CGGTGTGCGC GCGGCGCAC	239

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 985 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:177:

AGCAGCGCTA CCGGTGGCGC CGGGTTGCGC GCGCGCGCCG CGCGAGAAAG CCGAGCGGGC	60
GGCAACAGCG GTGTGGCGCG CACCAACCGC TTCGCGCGCG CGGCGGGTGC AGGCGGCAAG	120
GGCGCGACCG GAGGTGGCGG CGGGTCCGCG GCGGACAACC CCACCGGTGC TGGTTTCGCC	180
GGTGGCGCGG CGCGACACAG TGGCGCGGCG GCGCGCGCGG GGGCGGCGCG GCGGACCGGT	240
ACCGCGCGCA CCGCGCGCGT TGTGCGCGCG ACCGGTAGTG CAGGCATCGG CGGCGCGCGC	300
GGCGCGCGCG GTACCGCGCG CGATGGGGCG AGCGGTCTCG GCGTGGCGCT CTCGGCGCTT	360
GACGCGCGCG AAGCGCGCCA AGGCGGGCGC GCGCGCACCG CCGCGCGCGG CGGCATCAAC	420
GGGCGCGCGG GCGCGCGCGG CAACGCGCGG GACGCGCGCG ACGGCGCAAC CGGTGCGCGA	480
GGTCTGCGCG ACAACGCGCG GGTGCGCGGT GACGGTGGGG CCGGTGGCGC CGCGCGCAAC	540
GGCGCGCAAG CGGCGCTCGG CCGTACACCG AAGCGCGCGG ACGGCGCGCG CGCGCGCAAT	600
GGCGCGCAAG GGGCGCGCGG CGGTGCTGCG GGGCGCGCGG ACAACAATTT CAACGCGCGG	660
CAGGCTGGTG CCGCGCGCCA AGGCGCGCAA GCGCGCTTGG GCGCGCGCAAG CACCACTGTA	720
TGCGCTAGC CGCACCGCGG AAGCGCGTTC CAACAGCGCA CGATGCGCGC TTCCTTGGCG	780
CGTTGAGCCA GCGCGCGATC ACCTACGCTG ACGTACGCGA CGCCATAACG GCGCGCGAAG	840
CGATCTGTGG CGTGTGTGCT AAGCGCGTAA CAGGTCTACA GCTGGTGGCG GACCTGCGCG	900
AATACAATCC CGGGCTGACC ATGGACAGCG CGGCGCAAGT CCGTGGCGATC CGATCAGCGG	960
CGTACTGCGC CGAACACCTG GAACA	985

(2) INFORMATION FOR SEQ ID NO:178:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:178:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCGG ATTGCGCGGG TTTCGCCACC	60
CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCGGTTGC CGATGCGGCG	120
ATGAACGGGC GGCATCAAAAT TAGTGACAGG ACCTTTCAGT TTAGCGACGA TAATGGCTAT	180
AGCACTAAGG AGGATGATCC GATATGACCG AGTGGACAGC CGTGACGGTG GATCAGCAAG	240

AGATTTTGA	CAGGGGCAAC	GAGGTGGAGG	CCCCGATGGC	GGACCCACCG	ACTGATGTTC	300
GCATCAGACC	GTGGGAACTC	ACGGCGGCTA	AAAACGCCGC	CCACACGCTG	GTATTGTCCG	360
CCGACACAT	CGCGGAATAC	CTGGCGGCGG	GTGCCAAGA	CGGCGAGGCT	CTGGCGGACT	420
CGCTCGCAA	CGCGGCAAG	GGTATGCGG	AGGTTGATGA	GGAGGCTGCG	ACCGCGCTGG	480
ACAACGACCG	CGAAGGAACT	GTGAGGCGAG	AATCGGCCCG	GGCGCTCGGA	GGGACAGATT	540
CGGCGGAACT	AACCGATACG	CGAGGGGTGG	CCACGGCGCG	TGAACCCAAC	TTCTGCGATC	600
TCAAAGAAGC	GGCAGGAAG	CTCGAAACGG	GGACCAAGG	GGCATCGCTC	GGCAGCTTTC	660
CGGATGGGTG	GAACACTTTC	AACCTGACGC	TGCAAGGCGA	CGTCAAGCGG	TTCCGGGGGT	720
TTGACACTG	GGAGGGCGAT	CGCGCTACCG	CTTGGGAGGC	TTGCGTGGAT	CAACAACGCG	780
AATGGATACT	CCACATGGCG	AAATGAGCG	CTCGATGGC	CAAGCAGGCT	CAATATGTGG	840
CGCAGCTGCA	CGTGTGGCT	AGCGGGGAAC	ATCCGACTTA	TGAAGACATA	GTCCGGGCTG	900
AACGGCTTTA	CGCGGAAAC	CGTTGGGCTC	GGGACCAAT	TCTCCGGGTG	TACCGGAGCT	960
ATCAGCAGAG	GTGCGAGAG	GTGCTGACCG	AATACAACAA	CAAGGCAGCG	CTGGAACCGG	1020
TAAACCGCGC	GAAGGCTCGC	CGCGCCATCA	AGATCGACCC	CGCCCGGCTT	CCGCAAGAGC	1080
AGGATTTGAT	CGCTGGGCTC	CTGATGGCGG	CGCTGACCG	CTCGGTTGTC	ACTCCGGGTA	1140
CGGGATGGCC	AGCGGACCGG	ATGGTTCCGC	CTACCGGATC	CGCGGTTGGT	GGCTTCTCTG	1200
CTGACACCGC	GGCGGAGCTG	ACGTGGGCTG	GGCGGGAAGC	CGCAGCGCTG	TGCGGGGAGC	1260
TGGGGGTCAA	AGCGGCATCG	CTCGGTGGCG	GTGGAGGCGG	CGGGGTGCGG	TGCGCGCGCT	1320
TGGATCGCGC	GATCGGGGCG	GGCGAATCGG	TGCGGCGCGC	TGGCGCTGGT	GACATTGCGG	1380
GGTTAGGCCA	GGGAAGGGCG	GGCGGCGCGG	CGCGCTGGG	CGCGGCTGGC	ATGGGAATGC	1440
CGATGGGTGC	CGCGCATCAG	GGACAAGGGG	GGCGCAAGTC	CAAGGGTTCT	CAGCAGGAAG	1500
ACGAGGGGCT	GTACACCGAG	GATCGGGCAT	GGACCGAGGC	CGTCATTGGT	AACCGTCGGC	1560
GGCAGGACAG	TAAAGGATCG	AAGTGAACAT	GGACGAATTG	GACCGGATG	TGCGCGGGGC	1620
GTGACGCTG	CGCGGGGGGT	TTGATCGCG	CGTAGACGGG	ACGCTCAATC	AGATGAACAA	1680
CGGATCGCTC	CGCGCCACCG	ACGAAGCGGA	GACCGTCGAA	GTGACGATCA	ATGGCGACCA	1740
GTGCTCACT	GGCTCTGGCA	TGGAAGATGG	TTTGCTGAAG	AAGCTGGGTG	CGGAGGCGGT	1800
GGCTCAGCGG	GTCAACGAGG	CGCTGCACAA	TGCGCAGGCT	CGGCGCTCGG	CGTATAACGA	1860



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CGCGCGCGGCGC GAGCAGCTGA CGCGTGCCTT ATCGGCGATG TCCGCGCGGA TGAACGAGG 1920
AATGGCGCTAA GCGCATTTT GCGGTGGTAG CGACTACGCA CGCAATGAGC GCGCAATGC 1980
GGTCATTCAG CGCGCGCGAC ACGCGGTGAG TACGCAATGT CAATGTTTTT ACATGGATCG 2040
GCGGGGTTCG GAGGGCGCCA TAGTCTGGT CGCAATATT GCGCGAGCTA GCTGGTCTTA 2100
GGTTCGCTTA CGCTGGTTAA TTATGACGTC CATTACCA 2118

```

## (3) INFORMATION FOR SEQ ID NO:179:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```

Met Thr Glu Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
 1           5           10           15
Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
 20           25           30
Pro Ile Thr Pro Cys Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Glu
 35           40           45
Leu Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
 50           55           60
Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala
 65           70           75           80
Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
 85           90           95
Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100           105           110
Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115           120           125
Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
130           135           140
Gln Gly Ala Ser Leu Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn
145           150           155           160
Leu Thr Leu Gln Gly Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp
165           170           175
Glu Gly Asp Ala Ala Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg
180           185           190

```

Gln Trp Ile Leu His Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln  
 195 200 205  
 Ala Gln Tyr Val Ala Gln Leu His Val Trp Ala Arg Arg Glu His Pro  
 210 215 220  
 Thr Tyr Glu Asp Ile Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro  
 225 230 235 240  
 Ser Ala Arg Asp Gln Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg  
 245 250 255  
 Ser Glu Lys Val Leu Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro  
 260 265 270  
 Val Asn Pro Pro Lys Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro  
 275 280 285  
 Pro Pro Gln Glu Gln Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser  
 290 295 300  
 Asp Gly Ser Gly Val Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met  
 305 310 315 320  
 Val Pro Pro Thr Gly Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala  
 325 330 335  
 Ala Gln Leu Thr Ser Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp  
 340 345 350  
 Val Ala Val Lys Ala Ala Ser Leu Gly Gly Gly Gly Gly Gly Val  
 355 360 365  
 Pro Ser Ala Pro Leu Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg  
 370 375 380  
 Pro Ala Gly Ala Gly Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly  
 385 390 395 400  
 Gly Gly Ala Ala Leu Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala  
 405 410 415  
 Ala His Gln Gly Gln Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu  
 420 425 430  
 Asp Glu Ala Leu Tyr Thr Glu Asp Arg Ala Trp Thr Glu Ala Val Ile  
 435 440 445  
 Gly Asn Arg Arg Arg Gln Asp Ser Lys Glu Ser Lys  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:180:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

Ala Gly Asn Val Thr Ser Ala Ser Gly Pro His Arg Phe Gly Ala Pro
 1           5           10           15

Asp Arg Gly Ser Gln Arg Arg Arg Arg His Pro Ala Ala Ser Thr Ala
 20           25           30

Thr Glu Arg Cys Arg Phe Asp Arg His Val Ala Arg Gln Arg Cys Gly
 35           40           45

Phe Pro Pro Ser Arg Arg Gln Leu Arg Arg Arg Val Ser Arg Glu Ala
 50           55           60

Thr Thr Arg Arg Ser Gly Arg Arg Asn His Arg Cys Gly Trp His Pro
 65           70           75           80

Gly Thr Gly Ser His Thr Gly Ala Val Arg Arg Arg His Gln Glu Ala
 85           90           95

Arg Asp Gln Ser Leu Leu Leu Arg Arg Gly Arg Val Asp Leu Asp
100           105           110

Gly Gly Gly Arg Leu Arg Arg Val Tyr Arg Phe Gln Gly Cys Leu Val
115           120           125

Val Val Phe Gly Gln His Leu Leu Arg Pro Leu Leu Ile Leu Arg Val
130           135           140

His Arg Glu Asn Leu Val Ala Gly Arg Arg Val Phe Arg Val Lys Pro
145           150           155           160

Phe Glu Pro Asp Tyr Val Phe Ile Ser Arg Met Phe Pro Pro Ser Pro
165           170           175

His Val Gln Leu Arg Asp Ile Leu Ser Leu Leu Gly His Arg Ser Ala
180           185           190

Gln Phe Gly His Val Glu Tyr Pro Leu Pro Leu Leu Ile Glu Arg Ser
195           200           205

Leu Ala Ser Gly Ser Arg Ile Ala Phe Pro Val Val Lys Pro Pro Glu
210           215           220

Pro Leu Asp Val Ala Leu Gln Arg Gln Val Glu Ser Val Pro Pro Ile
225           230           235           240

Arg Lys Val Arg Glu Arg Cys Ala Leu Val Ala Arg Phe Glu Leu Pro
245           250           255

```

Cys Arg Phe Phe Glu Ile His Glu Val Gly Phe Thr Gly Arg Gly His  
 250 265 270

Pro Arg Arg Ile Gly  
 275

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Arg Val Ala Ala Ser Phe Ile Asp Trp Leu Asp Ser Pro Asp Ser Pro  
 1 5 10 15  
 Leu Asp Pro Ser Leu Val Ser Ser Leu Leu Asn Ala Val Ser Cys Gly  
 20 25 30  
 Ala Glu Ser Ser Ala Ser Ser Ser Ala Arg Ser Gly Asn Gly Ser Arg  
 35 40 45  
 Trp Thr Ser Met Pro Ser Gly Thr Arg Pro Gly Pro Arg Arg Ala Thr  
 50 55 60  
 Ser Arg Asp Asp Arg Arg Ser Ala Thr Ser Val Ile Pro Ser Arg Arg  
 65 70 75 80  
 Ser Val Ala Pro Arg Ala Glu Phe Gly Thr Arg Leu Ala Ser His Arg  
 85 90 95  
 Ala Ser Pro Ser Asn Ala Cys Pro Val Arg Ile Val Thr Ser Ala Ser  
 100 105 110  
 Gly Arg Pro Ile Ser Ser Pro Pro Ile Val Arg Ser Arg Ser Cys Val  
 115 120 125  
 Asp Lys Asn Gly Arg Arg Cys Ala Ser Gly Tyr Arg Arg Leu Asn Arg  
 130 135 140  
 Ala Arg Ser Ser Ser Ile Ala Ala Arg Cys Arg Thr Ile Gly Thr Phe  
 145 150 155 160  
 Arg Arg Ser Arg Tyr Ser Ala Ser Met Arg Val Ser Thr Asn Ser Pro  
 165 170 175  
 His Val Thr His Gly Val Ala Pro Gly Val Thr Arg Arg Ile Gly Gly  
 180 185 190

(2) INFORMATION FOR SEQ ID NO:182:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Gln Glu Arg Pro Gln Met Cys Gln Arg Val Ser Glu Ile Glu Pro Arg  
 1 5 10 15  
 Thr Gln Phe Phe Asn Arg Cys Ala Leu Pro His Tyr Trp His Phe Pro  
 20 25 30  
 Ala Val Ala Val Phe Ser Lys His Ala Ser Leu Asp Glu Leu Ala Pro  
 35 40 45  
 Arg Asn Pro Arg Arg Ser Ser Arg Arg Asp Ala Glu Asp Arg Arg Val  
 50 55 60  
 Ile Phe Ala Ala Thr Leu Val Ala Val Asp Pro Pro Leu Arg Gly Ala  
 65 70 75 80  
 Gly Gly Glu Ala Asp Gln Leu Ile Asp Leu Gly Val Cys Arg Arg Gln  
 85 90 95  
 Ala Gly Arg Val Arg Arg Gly Gln Glu Leu His His Arg His Arg His  
 100 105 110  
 Gln Gly Ala Ala Pro Asp Leu Arg Arg Arg Arg Arg His Arg Arg Val  
 115 120 125  
 Gln Gln His Arg Arg Leu Gln Arg Val Arg Gln Leu Arg Arg Tyr Val  
 130 135 140  
 Gln Thr Ala His His Arg Arg Phe Ala Arg Thr Asp Arg Val Arg His  
 145 150 155 160  
 His Val Arg Gly Pro Ser Asn His Arg Arg Arg Arg Val Tyr Arg Gly  
 165 170 175  
 Arg His Ser Gly Ala Gly Gly Cys Pro Ala Gly Gly Ala Gly Ser Val  
 180 185 190  
 Gly Gly Ser Ala  
 195

## (2) INFORMATION FOR SEQ ID NO:183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183.

Val Arg Cys Gly Thr Leu Val Pro Val Pro Met Val Glu Phe Leu Thr			
1	5	10	15
Ser Thr Asn Ala Pro Ser Leu Pro Ser Ala Tyr Ala Glu Val Asp Lys			
20	25	30	
Leu Ile Gly Leu Pro Ala Gly Thr Ala Lys Arg Trp Ile Asn Gly Tyr			
35	40	45	
Glu Arg Gly Gly Lys Asp His Pro Pro Ile Leu Arg Val Thr Pro Gly			
50	55	60	
Ala Thr Pro Trp Val Thr Trp Gly Glu Phe Val Glu Thr Arg Met Leu			
65	70	75	80
Ala Glu Tyr Arg Asp Arg Arg Lys Val Pro Ile Val Arg Gln Arg Ala			
85	90	95	
Ala Ile Glu Glu Leu Arg Ala Arg Phe Asn Leu Arg Tyr Pro Leu Ala			
100	105	110	
His Leu Arg Pro Phe Leu Ser Thr His Glu Arg Asp Leu Thr Met Gly			
115	120	125	
Gly Glu Glu Ile Gly Leu Pro Asp Ala Glu Val Thr Ile Arg Thr Gly			
130	135	140	
Gln Ala Leu Leu Gly Asp Ala Arg Trp Leu Ala Ser Leu Val Pro Asn			
145	150	155	160
Ser Ala Arg Gly Ala Thr Leu Arg Arg Leu Gly Ile Thr Asp Val Ala			
165	170	175	
Asp Leu Arg Ser Ser Arg Glu Val Ala Arg Arg Gly Pro Gly Arg Val			
180	185	190	
Pro Asp Gly Ile Asp Val His Leu Leu Pro Phe Pro Asp Leu Ala Asp			
195	200	205	
Asp Asp Ala Asp Asp Ser Ala Pro His Glu Thr Ala Phe Lys Arg Leu			
210	215	220	
Leu Thr Asn Asp Gly Ser Asn Gly Glu Ser Gly Glu Ser Ser Gln Ser			
225	230	235	240
Ile Asn Asp Ala Ala Thr Arg Tyr Met Thr Asp Glu Tyr Arg Gln Phe			
245	250	255	
Pro Thr Arg Asn Gly Ala Gln Arg Ala Leu His Arg Val Val Thr Leu			
260	265	270	
Leu Ala Ala Gly Arg Pro Val Leu Thr His Cys Phe Ala Gly Lys Asp			
275	280	285	

Arg Thr Gly Phe Val Val Ala Leu Val Leu Glu Ala Val Gly Leu Asp  
290 295 300

Arg Asp Val Ile Val Ala Asp  
305 310

(2) INFORMATION FOR SEQ ID NO:184:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CTCTGCGGA TTGCGCAGCA GCTGAGCAGC CCAAGGGGGC GTTCGGCGAA GTGATCGAGG	60
CATTGCGCGA CCGGGTGGCC GCGAAGGATA AGCAATCAA CACCAAGCTG AACAGCTGT	120
CGCAGGGGTT GAAGGCTTGA AATGAGGGCC GCGGCGACTT CTTCGGGCTG GTACGGAGCC	180
TGCGGCTATT CGTCAACGCG CTACATCAGG ACGACCAACA GTTCGTGCGG TTGAACAGAA	240
AGCTTGCGGA GTTCACGGAG AGGTGAGCTC ACTGGGATGC GGACCTGTGC AACGCCATCC	300
AGCAATTCGA CAGCTTGCTC GCGCTGCGCC GCGCTTCTTT CCGCAAGAAC CCGGAGGTGC	360
TGACGCATGA CGTCAATGAT CTCGGGAGCG TGACCAAGCA GTTGCTGCGG CCGGATCCCT	420
TGGATGGGTT GGAGACGGTC CTGCGAGATC TCCCGAGGCT GCGGGCGAAC ATTAACGAGC	480
TTACGATGCG GACACAGCTT GCGTGGTGT CCGTTTCCGC GTTCACGAAT TTGCGCAAGC	540
CGATGGAGTT CATCTCGAGC TCGATTGAGG CCGGTAGCGG GCTGGTTAT CAAGAGTCGG	600
CGGAAGCTTG TGCGAGTAT CTCGGCGGAG TCGTCGATGC GATCAAGTTC AACTACTTTC	660
CGTTGCGGCT GAACGTGGCC AGCAGCGGCT CGACACTGCC TAAAGAGATC GGTACTCTCG	720
AGCGCGCGCTT CGAGCGCGCC AACGGGTACA AGGACACGAC GGTGCGCGGC ATCTGCTGTC	780
CGGATACGCC GTTGTCACAC CCGAACACGC AGCGCGGTTG GGTGCTGCCA CCGCGGATGC	840
AAGGGTTTCA GGTGGGAGTG ATCAGCGCAG GTTTGCTGAC GCGGAGTCCG GTGGCGGAAC	900
TGATGGGTGG TCGGATATC GCGGCTCGGT CGTCAGGGCT GCAAAACCGCG CCGGAGCCCC	960
CGAATGCGTA CGAGAGATAC CCGGTGCTGC CGGGATCGG TTACAGGCC CCACAAGTGC	1020
CGATACAGCC CCGGCTCTCT GGGCGCGAGC TAATCCCGGG TCGGCTGCCA CCGGTCTTGG	1080
CGCGATCGTT GTTCCCAAGA GATCGCGCGG CAGGCTCGGA AAAGTTGAGC TACATGCGCC	1140

TCTTTTGGCT GTGCGCGGCG CTGCGGACCT TCTTTTGGG GGTGTGATCT AGCCCCGGCC	1290
GTGGAACGAT GCGCGATCGG CACGTGTTGA TACCGGCGAT CACCGGCGTG GCGTTGATCG	1260
CGGCAATCGT CGCACATCGG TGGTACCGCA CAGAACATCC GCTCATAGAC ATGCGGTTGT	1320
TGCAGAACCG AGCGGTGCGG CAGGCGAACA TGACGATGAC GGTGCTCTCC CTCGGGCTGT	1380
TTGGCTCCTT CTGCTGCTC GCGAGCTACC TCCAGCAAGT GTTGACCGA TCACCGATGC	1440
AATCGGCGGT GCATATCATC CCACAGCGCG TCGTGCCAT GCTGCGGATG CGGATCGCGG	1500
GAGCGATGAT GGACCGACCG GACCGCGCA AGATCGTCT GGTGCGGATC ATGCTGATCG	1560
CTCGCGGCTT GCGCACCTTC GCTTTTGGTG TCGCGCGGCA AGCGGACTAC TTACCGATTC	1620
TGCGGACCGG GCTGGCAATC ATGGGCGATG GCATGGGCTG CTCGATGATC CCAGTGTCCG	1680
GCGCGGCGCT GCAGACCGTG GCGCGACATC AGATGCTCG GGTTCGACG CTGATCAGCG	1740
TCAACCGAGC GGTGGCGGCT TCGATAGGGA CGCACTGAT GTCGGTGCTG CTCGACTACC	1800
AGTTCAATCA CAGCGAAATC ATCGCTACTG CAAGAAAGT CGCACTGACC CCAGAGAGTG	1860
GCGCGGCGCG GCGGCGCGCG GTTGACCTTT CTTGCTTACC GCGCGAAACC AACTTCGCGG	1920
CCCAACTGCT GCATGACCTT TCGCAGCGCT ACGCGTGGT ATTCTGATA GCGACCGCGC	1980
TAGTGTGTCT GACGCTGATC CCGCGCGCAT TCTGCGGAA ACAGCAGGCT AGTCATCGAA	2040
GAGGACCGTT GCTATCGGCA TGAGCTGTCT TT	2072

## (2) INFORMATION FOR SEQ ID NO:185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:185:

TCACCCCGGA GAAGTCCTTC GTGACGACC TGGACATGCA CTCGCTGTG ATGGTCGAGA	50
TGCGCGTGCA GACCGAGGAC AAGTACGGCG TCAAGATGCC CGACGAGGAC CTCGCGGTC	120
TGCTTACCTT CGGTGACGTT GTGCGCTACA TCCAGAACTT CGAGGAAGAA AACCCGAGG	180
CGGCTCAGCG GTTGCGCGCG AAGATTGAGT CCGAGAACCC CGATGCGGCA CGAGCAGATC	240
GGTGCTTTTC ACCGCATCG CAAGGTGCGG AGCGCGCTCG TCTCTTTGCA CGCTCAGCCA	300
GCTTGGCGTG TCGCGCGCTT CCAGCAAGTG TTCCGACGAC ACCAAGGGAC CCGCGCGAAA	360
GCTGACTGAT CCGCGGACCA CATAGTCGAT GCGACCGTGG CTCACAATTG CCGCGGCTCC	420



GAGTTGGCGG	GGGCCGAATT	GGGGCATTGC	GTGGAAGGCC	AGCGGATCCC	GGCGCCCGCC	480
CGCGTGCTCT	GGTGTTTTGG	GGCGCCGGAT	GGCCACGACC	AGAACGACGA	TGGCGCGGAT	540
GAACAGCGCC	ACGGCAATCA	CGACCGACAG	ATTTCCTCAC	CATACCTCT	CGTACCGCTG	600
CGCCCGCGTT	GGTGGATCGG	TGCATATCG	ATGGCGCGGT	TTAAGGTAA	AGCTTTCCCG	660
GGACCGGGGG	TCAACACGGG	CGAGTTGTCC	GGCGGGGAAC	CGCGCAGGTC	TGGCGCCCGG	720
TCACCGCAGC	TCAGTGTGTC	ACCATCCGGG	TGTGGGTGAG	CGTCAACTC	AAACACACTC	780
AACCGCAACG	GTTCCTCAGG	TCACGAGGTC	AACCTCGACC	CGCAATCGCT	CGTACGTTTC	840
GACCGCGCGC	AGGTGGCGAG	TCAGCAGGTT	TGCGCCGGCA	CGTTTGGCGG	TGAAGCGGAC	900
CAGGGGATCG	TAGGTTCCGC	CACCGGTGAC	ATCGTGGCTG	CGCAGGTGGT	CGGTCAAGCC	960
CGGATATGAG	CAGGCATCCA	GTGCCAGGTA	GTTCCTGGAG	GTGATGTCCG	CGAAGTAGGC	1020
GTGACCGCCA	ACAGGGGCTA	TACGATCGGG	CGGTGGTAGC	CGGTCGAAGA	CGGAATAGGT	1080
TTCCACAGCC	CGGTGGCGGA	TCAGATGGAC	GCCACGGTTG	AGCGCGCGCA	CGGCGGCTTC	1140
GTGGCGTTCC	TGGCAGGTCC	CGAATCGGGC	AACCGACACG	GTGGTGTCTG	GTGCGATCAC	1200
CGCGGTGTCC	GATCGAGCGT	TTCCCGAAGC	ATTTCGTCCG	TCAACGGGGG	CAGGGGAGCT	1260
TTTGGCGCTG	CGACGAGAAC	CGAGCGTTCC	CGAACGAGTT	CGACACCGGT	CGGGCGCTGC	1320
TCAATCTCGA	TGCGCCCATC	GGGCTCGGTG	ATCTCCACCT	GGTCTTTCCG	CGCGAAGCTA	1380
AGCGCGTCCG	GAATCCGCTT	GGGAATCACC	AGACGTCTCG	CGACATCGAT	GGTTGTTCGC	1440
ATGGTAGGAA	ATTTACTATC	CGACGTTCCA	TAGGCGTGTG	CTCGCGCGGA	TGTGGGACG	1500
ATCGCGTAGC	GTATCGAAGC	ATTGTTTCGG	AAATGGCTGA	GGGAGCGTCC	GGTCCGGGTG	1560
ATGGGTGTCC	ATCCCGGGTT	GACCGGATCC	GGGCTGTCCG	TCATCGAGAG	TGGGGTGGTT	1620
CGCGAGCTCA	CGCGCTCGGA	TGTGACGCTG	GTGCGCACAC	CGTGGGATCG	GGCTTTGGCG	1680
CAGCGCTGCT	TGGCCATCAG	CGATGCCGTC	GAGCACTGCG	TGGACACCCA	TGATCCGGAG	1740
GTGGTGCCTA	TGGAACGGGT	GTTCCTCAG	CTCAACGTGA	CGACGGTGAT	GGGACCGCGG	1800
CAGCGCGCGG	CGGTGATCGC	GTGGCGGGCT	GCCAAACGTC	GTGTGCAAGT	CGATTTCGAT	1860
ACCGCCGCGG	AGGTCAAGGC	GGCGGTCACT	GGCAACGGTT	CGCGAGACAA	GGCTCGAGTC	1920
ACC						1923

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

CTGGCGTGGC AGTGTACACG GCGATATGAC GTGGGCATTC AATTTCGCGG CCGGCGCGGA      60
CCGCTCGCCA CCAATCTGG ACCACCCCGT GGTCAATTC GCGAGGTTC CCAAGTGGT      120
GCCAATGTC GTGCTGGGT TCTTGAACGA AGGCGTGGG TATCGGTTC GCTACCGCCA      180
AACAAGGCGA GTCCAGGAAT CCGTCCCGC GCGCGCGATT CCGAGCGCA TGTGTAGCC      240
GGGATGGTT GAGACGTAA GGTGGCTAG GTCAAAACC GCCCAGGGC GGTGAGCGG      300
GTCATGSCA GCGAAATTA AAAACCCCG ATATTGTGG CGGATGTCA TAGGATGCTG      360
AGTGCTTGT GTTCTGTGT TAGGCATTA GTGTGGATGT GTTGAGACC TGGCTGGA      420
GGGACAAAG TGTCTTTCG TCTTGTTCG CTTTGGCGG CCGAGCGGT GTTGGCGAAA      480
CGGCTGTGAT CGGGAATGCT CGGCGGTTC TCGGTTCGC TCGCTGGG AGTGGCTGTG      540
CGACCGGATG ATTATGACCA GTGGCGGCT CCGCGGAGG AGCGCGCGA TGTGATGTC      500
CAGCGCGCG AAGGGCGGA CCGAGGCGC CGGCGATGG ACGAGTGGG TGAGTGGCAG      560
GTGTGGAAG AGTGGGTGG GAGAAACCT GAACCCCGT TTGAGTGGT ACGAGTAGC      720
AGGAGCTGA TCGGCATTC TCGGCGCGC GGTAGGAGA GGGGCGCGG ACTGTGTTA      780
TTGAGGAGT GATCGCGGT CTCGTGTTT CCGCGCGCG CTATGACAC AGTCAATGTG      840
GATGACAAGT TACAGGTATT AGGTGAGGT TACACAGGA GACAGGCAAC ATGGCAACAC      900
GTTTTATGAC GATTCGCGC GCGATGCGG ACATGCGGG CCGTTTCAG GTGCACGCC      960
AGAGGTGGA GACAGAGCT CCGCGATGT GCGCTCGCG GCAAAACAT TCGGNGCGG      1020
GCTGAGTGG CATGCGCGG GCGACCTGC TAGAC      1055

```

## (2) INFORMATION FOR SEQ ID NO:187:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:187:

```

CGCGCTGTT GTTGACATG TCGCGCGCG CCGCTCGAC GCACTGGCG GTGCTGTG      60

```

```

TCCGGGCTGA CCACGGGGAT CCGCGAACCA TCCGAGTCA CCTCGCAATG ATCCACCTCG      120
CGCAGCTGGT CACCCAGCCA CCGGGGCTG TCGACAGCG CCGCATCAC CTGGGTATAG      180
CGGTCCGCC CCAGCGGAGG GAAGTTTAG TACTGCCCA CCACCTGGT ACCGGGACGG      240
GAGAAGTTCA GGTGAAGGT CGGCATCTCG CCGCCGAGGT ACTTCACCGG GAAAACAGA      300
TCTTCGGCCA GTTCTCGGG CCGCGCCAC ACGACAAAC CGACCGCGG ATAGGTGAG      359

```

## (2) INFORMATION FOR SEQ ID NO:188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```

AACGGGCCCC TCGGCACCGG TCTCTAAGG GCTCTGTTG GTGCGATGAA GTGCTGGAAQ      60
GATGCATCTT GGCAGATTC CCGCAGAGCA AACACGCCG TACTCTAGT CCGAGTGGCC      120
CGCAAAAGTC CTGGAATAA TCGTAACCG GAGCGCCAA CCGGTCTCC TTGCTAAGC      180
TGGCGAACC ACTTGAGGTT CCGGGACTCC TTGACGTCA GACCGATTC TTGAGTGGC      240
TGATCGTTC GCGCGCTCG CGCGAATCG CCGCGAGCG GGTGATATC AACCCAGTGG      300
GTGCGCTGGA AGAGGTGCTC TACGAGCTGT CTCGATCGA GGAATTCTCC      350

```

## (2) INFORMATION FOR SEQ ID NO:189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

```

Glu Gln Pro Lys Gly Pro Phe Gly Glu Val Ile Glu Ala Phe Ala Asp      10
1           5           10           15
Gly Leu Ala Gly Lys Gly Lys Gln Ile Asn Thr Thr Leu Asn Ser Leu      20
20          25          30
Ser Gln Ala Leu Asn Ala Leu Asn Glu Gly Arg Gly Asp Phe Phe Ala      35
35          40          45
Val Val Arg Ser Leu Ala Leu Phe Val Asn Ala Leu His Glu Asp Asp      50
50          55          60

```

Gln Gln Phe Val Ala Leu Asn Lys Asn Leu Ala Glu Phe Thr Asp Arg  
 55 70 75 80  
 Leu Thr His Ser Asp Ala Asp Leu Ser Asn Ala Ile Gln Gln Phe Asp  
 85 90 95  
 Ser Leu Leu Ala Val Ala Arg Pro Phe Phe Ala Lys Asn Arg Glu Val  
 100 105 110  
 Leu Thr His Asp Val Asn Asn Leu Ala Thr Val Thr Thr Thr Leu Leu  
 115 120 125  
 Gln Pro Asp Pro Leu Asp Gly Leu Glu Thr Val Leu His Ile Phe Pro  
 130 135 140  
 Thr Leu Ala Ala Asn Ile Asn Gln Leu Tyr His Pro Thr His Gly Gly  
 145 150 155 160  
 Val Val Ser Leu Ser Ala Phe Thr Asn Phe Ala Asn Pro Met Glu Phe  
 165 170 175  
 Ile Cys Ser Ser Ile Gln Ala Gly Ser Arg Leu Gly Tyr Gln Glu Ser  
 180 185 190  
 Ala Glu Leu Cys Ala Gln Tyr Leu Ala Pro Val Leu Asp Ala Ile Lys  
 195 200 205  
 Phe Asn Tyr Phe Pro Phe Gly Leu Asn Val Ala Ser Thr Ala Ser Thr  
 210 215 220  
 Leu Pro Lys Glu Ile Ala Tyr Ser Glu Pro Arg Leu Gln Pro Pro Asn  
 225 230 235 240  
 Gly Tyr Lys Asp Thr Thr Val Pro Gly Ile Trp Val Pro Asp Thr Pro  
 245 250 255  
 Leu Ser His Arg Asn Thr Gln Pro Gly Trp Val Val Ala Pro Gly Met  
 260 265 270  
 Gln Gly Val Gln Val Gly Pro Ile Thr Gln Gly Leu Leu Thr Pro Glu  
 275 280 285  
 Ser Leu Ala Glu Leu Met Gly Gly Pro Asp Ile Ala Pro Pro Ser Ser  
 290 295 300  
 Gly Leu Gln Thr Pro Pro Gly Pro Pro Asn Ala Tyr Asp Gln Tyr Pro  
 305 310 315 320  
 Val Leu Pro Pro Ile Gly Leu Gln Ala Pro Gln Val Pro Ile Pro Pro  
 325 330 335  
 Pro Pro Pro Gly Pro Asp Val Ile Pro Gly Pro Val Pro Pro Val Leu  
 340 345 350  
 Ala Ala Ile Val Phe Pro Arg Asp Arg Pro Ala Ala Ser Gln Asn Phe

155	160	165
Asp Tyr Met Gly Leu Leu Leu Leu Ser Pro Gly Leu Ala Thr Phe Leu 370 375 380		
Phe Gly Val Ser Ser Ser Pro Ala Arg Gly Thr Met Ala Asp Arg His 385 390 395 400		
Val Leu Ile Pro Ala Ile Thr Gly Leu Ala Leu Ile Ala Ala Phe Val 405 410 415		
Ala His Ser Trp Tyr Arg Thr Glu His Pro Leu Ile Asp Met Arg Leu 420 425 430		
Phe Gln Asn Arg Ala Val Ala Gln Ala Asn Met Thr Met Thr Val Leu 435 440 445		
Ser Leu Gly Leu Phe Gly Ser Phe Leu Leu Leu Pro Ser Tyr Leu Gln 450 455 460		
Gln Val Leu His Gln Ser Pro Met Gln Ser Gly Val His Ile Ile Pro 465 470 475 480		
Gln Gly Leu Gly Ala Met Leu Ala Met Pro Ile Ala Gly Ala Met Met 485 490 495		
Asp Arg Arg Gly Pro Ala Lys Ile Val Leu Val Gly Ile Met Leu Ile 500 505 510		
Ala Ala Gly Leu Gly Thr Phe Ala Phe Gly Val Ala Arg Gln Ala Asp 515 520 525		
Tyr Leu Pro Ile Leu Pro Thr Gly Leu Ala Ile Met Gly Met Gly Met 530 535 540		
Gly Cys Ser Met Met Pro Leu Ser Gly Ala Ala Val Gln Thr Leu Ala 545 550 555 560		
Pro His Gln Ile Ala Arg Gly Ser Thr Leu Ile Ser Val Asn Gln Gln 565 570 575		
Val Gly Gly Ser Ile Gly Thr Ala Leu Met Ser Val Leu Leu Thr Tyr 580 585 590		
Gln Phe Asn His Ser Glu Ile Ile Ala Thr Ala Lys Lys Val Ala Leu 595 600 605		
Thr Pro Gln Ser Gly Ala Gly Arg Gly Ala Ala Val Asp Pro Ser Ser 610 615 620		
Leu Pro Arg Gln Thr Asn Phe Ala Ala Gln Leu Leu His Asp Leu Ser 625 630 635 640		
His Ala Tyr Ala Val Val Phe Val Ile Ala Thr Ala Leu Val Val Ser 645 650 655		

Thr Leu Ile Pro Ala Ala Phe Leu Pro Lys Gln Gln Ala Ser His Arg  
 560 565 570

Arg Ala Pro Leu Leu Ser Ala  
 575

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Thr Pro Glu Lys Ser Phe Val Asp Asp Leu Asp Ile Asp Ser Leu Ser  
 1 5 10 15  
 Met Val Glu Ile Ala Val Gln Thr Gln Asp Lys Tyr Gly Val Lys Ile  
 20 25 30  
 Pro Asp Glu Asp Leu Ala Gly Leu Arg Thr Val Gly Asp Val Val Ala  
 35 40 45  
 Tyr Ile Gln Lys Leu Glu Glu Gln Asn Pro Gln Ala Ala Gln Ala Leu  
 50 55 60  
 Arg Ala Lys Ile Glu Ser Glu Asn Pro Asp Ala Ala Arg Ala Asp Arg  
 65 70 75 80  
 Cys Val Ser Pro Thr Ser Gln Ala Arg Asp Ala Arg Arg Pro Leu Ala  
 85 90 95  
 Arg Ser Ala Arg Leu Ala Cys Arg Arg Leu Pro Ala Ser Val Pro Thr  
 100 105 110  
 Thr Arg Arg Asp Pro Arg Glu Arg  
 115 120

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Leu Ala Cys Gln Cys His Arg Arg Tyr Asp Val Gly Ile Gln Phe Arg  
 1 5 10 15  
 Gly Pro Ala Gly Pro Val Ala Thr Gln Ser Gly Pro Pro Gly Pro Ser

	20		25		30
Ile Ala Glu Gly Arg Gln Val Arg Ala Gln Cys Gly Ala Gly Phe Leu					
35		40		45	
Glu Arg Arg Pro Ala Val Ser Gly Ala Leu Pro Pro Asn Asn Ala Ser					
50	55		60		
Pro Gly Ile Arg Ser Arg Ala Ala Asp Ser Gln Arg His Leu Leu Ala					
65	70		75		80
Gly Asp Gly Ser Asp Val Thr Val Gly					
	85				

## (3) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Ala Ser Leu Leu Ala Tyr Ser Ala Ala Ala Ala Ser Thr Ala Leu Ala					
1	5	10	15		
Val Ala Cys Val Arg Ala Asp His Arg Asp Arg Arg Thr Ile Arg Asp					
20	25	30			
His Leu Ala Met Ile His Leu Ala Gln Leu Val Thr Gln Pro Pro Gly					
35	40	45			
Gly Val Arg Gln Arg Leu His His Leu Gly Ile Ala Val Ala Pro Gln					
50	55	60			
Pro Gln Glu Val Val Val Leu Ala His His Leu Val Thr Gly Thr Gly					
65	70	75		80	
Glu Val Gln Gly Glu Gly Arg His Val Ala Ala Glu Val Val Asp Pro					
	85	90	95		
Glu Asn Gln Ile Leu Arg Gln Val Leu Gly Pro Ala Pro His Asp Lys					
100	105	110			
Pro Asp Ala Gly Ile Gly Gln					
	115				

## (2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Arg Ala Arg Gly His Arg Ser Ser Lys Gly Ser Arg Trp Ser His Glu  
 1 5 10 15  
 Val Leu Glu Gly Cys Ile Leu Ala Asp Ser Arg Gln Ser Lys Thr Ala  
 20 25 30  
 Ala Ser Pro Ser Pro Ser Arg Pro Gln Ser Ser Ser Asn Asn Ser Val  
 35 40 45  
 Pro Gly Ala Pro Asn Arg Val Ser Phe Ala Lys Leu Arg Glu Pro Leu  
 50 55 60  
 Glu Val Pro Gly Leu Leu Asp Val Gln Thr Asp Ser Phe Gln Trp Leu  
 65 70 75 80  
 Ile Gly Ser Pro Arg Trp Arg Glu Ser Ala Ala Glu Arg Gly Asp Val  
 85 90 95  
 Asn Pro Val Gly Gly Leu Glu Glu Val Leu Tyr Glu Leu Ser Pro Ile  
 100 105 110  
 Glu Asp Phe Ser  
 115

## (12) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

TGCTACCGAG CAATCGCTTT GGTGACAGAT GTGGATGCCG GCGTCGCTGC TGCGATGGC 60  
 GTGAAGGCCG CGACGCTTT CCGCGCATTG GGGGAGAACA TCGAAGTGTG CAAAAGGCTG 120  
 GTGGGGGCCG CCAATGATCG GTTCGGCGAC GAGCGCACGT GCACGCACTG TCAACACGAC 180  
 GCGCGTGTTC GTTTGCCGTT CGAGCTGCCA TGAGGGTGGT GCTGACCGGC GCGGGCGGCT 240  
 TCATCGGGTC GCGGGTGGAT GCGGGCTTAC GGGCTGCGGG TCACGACGTG GTGGGCGTGG 300  
 AGCGCGTGGT GCGCGCGCGG CACCGGCCAA ACCCGGTGGT GCGACCGGCG TGCCAGCGGG 360  
 TCGACGTGGG CGACCGCCAG GCGGTGGCGG CGTTGTTGGC CGGTGTGGAT CTGGTGTGTC 420  
 AGCAGCGCGC CATGGTGGGT GCGCGGCTCA AGCGCGCGCA CGCAGCGGCT TATGCGCGCC 480  
 ACAACGATTT CCGCACCAAG GTGCTGCTGG CGCAGATGTT CGCGCGCGGG GTCCGCGGTT 540



TGTTGCTGCG	GTCTGTGATG	GTGGTTTACG	GGCAGGGGCG	CTATGACTGT	CCCCAGCATG	600
GACCGGTGCA	CCCGCTGGCG	CGCGGGCGAG	CGGACCTGCA	CAATGGGGTC	TTGAGCAGCT	660
GTTCCTCCGG	GTGCGGGGAG	CGAGTCATCT	GGCAATTGGT	CGACGAAGAT	GCCCCGTTGC	720
GGCCCCCGAC	CGTGTACGGC	CGACGAAGAC	CGCGCGAGAG	CACTACGGCG	TGCGGTGGTC	780
GGAAACGAAT	GGCGTTTCCG	TGTTGGCGTT	G			811

(2) INFORMATION FOR SEQ ID NO:195:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GTCCCCGAT	GTGGCCGAG	ATGACTTTG	GCACACCGG	CGTAGTAGTC	GAAGATATCG	60
GACTTTTGG	TCCCGGTGCG	GGGTATAGAG	ACCTGTGGCG	GTGGGTGAGC	GTACCCGTTT	120
GCTCGGAGCG	CGAACCCATG	CTTTCAACGT	AGCCTGTGCG	TCACACAAGT	CGCGAGCGTA	180
ACGTGACGCT	CAAAATATCG	GTGGAATTTT	GGCGTGACGT	TCCGCTCGCG	GACAATCAAG	240
GCATCTCAC	TTAGATCGCA	GGCATTTGGA	CGGGTTGAT	CGGCTTCGGG	CTGTGGAACG	300
TGCGGTGCA	GGTGTACAGC	GCTACCGCAG	ACCACGACAT	CAGGTTCCAC	CAGGTGCAGC	360
CGAAGGACAA	CGGACCGCAT	CGGTACAGCG	CGCTCTGCGA	GGCGTGTGCG	GAGGTGCTCG	420
ACTACCGCGA	TCTTGGCGCG	GCTTACGAGT	CGGCGGACGG	CTAAATGGTG	GCGATCACCG	480
AGGAGGACAT	CGCCAGCTTG	CTGGAAGAAC	CGAGCCGGGA	GATCGAGGTC	TTGGAGTTG	540
TCCCCCGCGC	CGACGTGGAC	CGGATGATGT	TGACCGCAGC	CTACTTTTTG	GAGCGTGATT	600
CGAAGTCTGC	GAAATCTAT	GTCTCTCTCG	CTAAGACACT	CGCGGAGACC	GACCGGATGG	660
CGATCTGGA	TGCGCCGAGC	GGCGTGAT	GCAGGAAAAA	TAGAGCGCGC	TATCCACCAT	720
TGCGGTGCGA	GCTGGGTAC	CACAAACGGT	AGAACGATCG	AGACATTTCC	GAGCTGAAGT	780
CGCGGCTAT	AGAAGCGGCT	CTCGCGGATT	ATCAAACGCA	AAATACGCTT	ACTGCTGCTA	840
TGCGGCGTGC	TCACCGGATC	CGAGTTTTTT	GGCAGGCTCC	ACCGCGTGCC	GGCGGACCTC	900
AAGTGGGCAT	GCATCGGAGC	CTTCCCGGGA	AACCGGTTCC	GGCGGGTCGG	CTCATCGGTT	960
CACTCT						966

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

CCGCACCGCC GGCATACCG CCAGCGCCAC GCTTACCGCC GTTTCGCGCG TTGCCCCCGT	60
TGCGCGCGGT CCGCGCGGCC CCGCGGATGG AGTTCTCATC GCGAAAAGTA CTGGCGTTGC	120
CACCGAGGCG GCGCTTGGCG CGCTCACCGC CAGCGCGCGC GACTCCACCG GCGCCACGGA	180
CTCGCGCGGT GCGACCGTTG CCGCGGTTGC CGATCAACAT GCGCGTGGCG CCGACCGTTG	240
CACCGACCGC ACGCGGTCGC CCGACCGCGC CGACACCAAG CGAGCTGCGC CCGGAGCGAC	300
CATCACCGAC TACGCCACCG AGCGCGCAGA CACCGAGGAC CGGCTCTTTC TGAACGTCG	360
CGGTGCGACG AGCGCGCGCG TTACCGCCAA CCGCACCGGC AACCGCGCGC CCGGCATCGC	420
CGCGCGCGCG GCGCTTGGCG CGTTTGGCGC GCTTGCAGAA CAACAAACCG CCGCGCGCGC	480
CTTTGCGCGC CGCGCGCGCG GTCCGCGCGC CGCGCGCGAC GCGAAGCGCG CTGCGCGCGT	540
TGCGCGCATC ACCACCGTTG CCGCGGACCA CATCGGGTTC TGCGTCGGCG TGTGGGCTGT	600
CAAAGCTGCG GATCGGACCG TTGCGCGCGC TTGCGCGCGC CGCTCGCGTG CGCGCGTCAC	660
CACGCTACCG AGCTCGCGCA CCGCGCGCAC GCTTGGCGCG ATCACCGAAT AGCAACCTGC	720
CGCGCGCAAG ATTGCGCGCA GTCGCGCGTG CCGCACGCTC GCGCGCGGAG CGCGCACTGC	780
CAGCGCGCTT ACCACGAAAA CGCGCGGTAC CACGCTAGA GGTGGCATG GCGATGTGTA	840
CGAAGCGCGC GCGTCGCGCG CGCGCGGTAC CACTCCCACT GCGCGCGGCT ACACCGTCGCG	900
ACCGCTTTCG ACCATCACCG CCAAGGCGCG TGCGAATGTC GCGCTGCGCG ACTGCGCGGT	960
CGCGCGGTTT GCGCGCGCGC CGACCGCGAG CGCGGTACCG GCGCTCACCA CCGGCACCGC	1020
CGGTGGCGTT GCGCGGCGCT GCGGTGCGCG TGCGACCGTC GCGCGCGGTC CGACCGGTGC	1080
GCTTGGCGCG AGTGGCATGG CGCGCGGTGC GCGCGTCGCG CGCGGTTTGA TGCGCGATGC	1140
CGGACACATG TGCGCGCGTG TCGCGCGTGC TGCGCGCGCG GCGCGCGGTC CGATTGACCG	1200
CGTTTGGCGC GCGGAGCGCG GCGCGCGCGC TACCAACCGC GCGCGCATGC CGGAACAGCG	1260
CGCGGTTGCG GCGCTTACCG CGCGCACCGC CGATGCGTGC GCGCACGCTG GTTGGCGCGA	1320
CACGCGCGTT GCGCGGTTG CCGCACCAAG ACTCGCGGTT CCGCACGCGA CGCGCGCGCG	1380

```

CGCGGTACC  AGCGGCCCCG  CGTTGCGCG  CATTGCGGAT  CAACCGCGCC  GCGCTTCGCG  1440
TGGCGCGGT  TTGACCGAAC  CGCGGAGCG  CGCGTTGCG  ACCGTGCGCA  AACAGCAACC  1500
CGCGCGCGCG  GCGAGCGTGC  CGCGGTGCG  TCGCGTGGC  GCGTTTCCG  ATCAACGGGC  1560
GCGCGAAAG  CGCGTGGTG  GCGCGATTC  CGCGAGCGG  CAGACTCGCG  TCAACAGCGG  1620
CTTCAGTGT  GCGATACCG  CGCGCGCGCG  CAGTCAACCG  CTGCGCAAA  TGCTGTGAA  1680
ACGCTGCGCG  CTGTACGCTG  AGCGCGTGT  ACTGCGCGCG  ATGCGCGCG  AACAAACCGG  1740
CAATGCGCG  CGACATTC  TCGCGAGCG  CAGCGAGCG  TTGCGTGTG  GCGATGCGCG  1800
CGCGCGCAT  AGCGCGCGT  ACTGCGAAC  CAATAGTGA  TAAATCGAA  GCGCGAGTTC  1860
CGAGCAGTG  CGCGTGGCG  ATCAGCAAG  ACACCTGCG  CCGCGGATA  CGCATATCG  1920
CGCGAGCGT  TCGCGAGCG  CGAGTGGCG  TTGCGTGTG  GCGTGGCGG  CCGTACTATG  1980
GCGCGAGCG  CGCGTGTGT  GATTGCGCG  GCGCGCGCG  TTGCGTGGG  AGTTGAAGAC  2040
GCGAGGACAG  GCGAGCGTG  GTGTAGCGT  GCGTCAAGT  GGAATGCGG  GTGCGCGCG  2100
AGATGAATG  GCGAGCGCG  ATCTCTTGT  TGCTGAGTG  CTCAGCGAG  AGTAGAGCG  2160
CGTCAAGCT  TGTCGGTGT  AACGCGCGG  AGCGAGTGT  CGCGCGTTC  CGTGCAGCG  2220
GCGTGGTG  CGGTAGCG  ATGCGTGT  CGATGATGA  CGAGTGTGT  TCGCGCGAG  2280
CATCTCGAA  CTGCTGTGA  CGCATGAT  TTGGAAGGT  GCGTAGCGAG  GAGTTACAG  2340
CGCGTGTGA  GATGCGAG  CGAGCG  2367

```

## (2) INFORMATION FOR SEQ ID NO:197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

Gln Pro Ala Gly Ala Thr Ile Ala Ala Ser Ser Pro Cys Ala Thr Val
 1             5             10             15
Gly Ala Gly Gly Gly Thr Gly Ser Pro Val Thr Thr Glu Thr Ala Ala
 20             25             30
Thr Thr Gly Arg Gly Gly Ser Gly Asp Val Tyr Glu Ser Ala Ala Ser
 35             40             45
Gly Ala Ala Ala Thr Thr Pro Thr Ala Gly Gly Tyr Thr Val Gly Pro
 50             55             60

```

Val Ala Thr Ile Thr Ala Lys Gly Ala Arg Asn Val Ala Leu Arg Asp  
 65 70 75 80  
 Ser Ala Val Ala Ala Val Ala Ala Ala Thr Gly Ser Gly Gly Thr  
 85 90 95  
 Ala Val Thr Thr Gly Thr Ala Gly Gly Leu Ala Arg Ala Cys Arg Arg  
 100 105 110  
 Gly Gly Thr Val Ala Ala Gly Ala Thr Gly Arg Arg Ala Gly Ser Ala  
 115 120 125  
 Met Ala Ala Arg Ala Ala Val Ala Ala Gly Leu Ile Thr Asp Ala Gly  
 130 135 140  
 His Ile Cys Arg Ala Val Pro Gly Ala Gly Arg Gly Ala Gly Arg Gly  
 145 150 155 160  
 Ile Asp Pro Val Cys Pro Gly Glu Ala Gly Ala Ala Gly Thr Thr Gly  
 165 170 175  
 Ala Ala Met Ala Glu Gln Pro Gly Val Ala Ala Val Thr Ala Arg Thr  
 180 185 190  
 Pro Asp Ala Cys Gly His Ala Gly Ala Ala Asp Thr Ala Val Ala Ala  
 195 200 205  
 Val Ala Pro Gln Pro Pro Pro Val Pro Thr Gly Thr Ala Gly Arg Ala  
 210 215 220  
 Gly Thr Thr Gly Pro Ala Val Ala Ala Val Ala Asp Gln Pro Gly Arg  
 225 230 235 240  
 Ala Ser Ala Ala Ala Gly Leu Thr Glu Pro Ala Ser Arg Ala Val Ala  
 245 250 255  
 Thr Val Ala Lys Gln Gln Pro Ala Gly Arg Ala Arg Leu Pro Gly Cys  
 260 265 270  
 Arg Pro Val Gly Ala Val Ser Asp Gln Arg Ala Pro Gln Lys Arg Leu  
 275 280 285  
 Gly Gly Arg Ile His Arg Thr Gln Gln Thr Pro Leu Asn Ser Gly Phe  
 290 295 300  
 Ser Ala Gly Ile Pro Thr Arg Gly Arg Ser Gln Arg Leu His Lys Leu  
 305 310 315 320  
 Leu Val Lys Arg Cys His Leu Tyr Ala Glu Arg Leu Ile Leu Pro Ser  
 325 330 335  
 Met Gly Pro Glu Gln Pro Arg Asn Arg Arg Arg His Phe Ile Gly Ser  
 340 345 350

Arg Ser His His Phe Arg Arg Arg Asp Arg Arg Gly Arg Ile Ser Arg  
 153 160 365

Ala His Leu Arg Thr Asn Ser Arg  
 370 375

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```

GGCCAAACG CCGCGCGGAT CCGCGCGGAC GAGCGCGCCT ACGACCGAG GTGGGCCGAG      60
GACGTGGCGG CGATGTTTGG CTACCATGCC GCGGCTTCGG CCGCGCTCTC GGCCTTGACA      120
CGGTTCCGCC AGCGCGCTGC GACCGTGGCG GCGCGCGGTC CGCTGGTCAG CCGCGCGCGG      180
GCTCAGGTGA CCACCGGGGT GTTCGCAAC CTGGCGTTGG CCAACGTGGG GAGAGGCAAC      240
GTCCGCAAGG GTAATGTCTG GAATCTCAAT CTCGGCTCGG CCAACATCGG CAACCGCAAC      300
ATCGCGAGCG GCAACATCGG CAGCTCCAAC ATCGGGTTTG GCAACGTGGG TCTCTGGTTG      360
ACCGCAGCGG TGAACACAT CGGTTTCGGG AACACCGGCA GCAACACAT CGGTTTGGGC      420
AACACCGGCA GCAACACAT CGGTTTCGGG AATACCGGAG ACCCGCAACCG AGGTATCGGG      480
CTACCGGTA CGGTTTCTT GGGGTTTCGG GCGCTGAAC CTGGCCACCG CAACATCGGT      540
GTGTTCAACT GGGGCACCGG AACGTTCGG ATCGGCAACT CGGTATCGGG GAATCGGGG      600
ATTGCAACT CGGCAACAG CTACAACACC GTTTTTCGCA ACTCGGCGCA GCGCCACACC      660
GGCTTCTTCA ACTCGGGAAT AGCCACACCC GCGCTCGGCA ACCCGGCAAA CTACAACACC      720
GGTAGCTACA ACCCGGCAAA CAGCAATACC GCGGCTTCA ACATGGGCCA GTACAACACC      780
GGCTACCTGA ACAGCGGCAA CTACAACACC GGCTTGGCAA ACTCGGCAAA TGTCAACACC      840
GGCGCTTGA TTAATGGCAA CTACAACACC GCGTTCTTGT GCGCTGGGCA CCAACCAAGG      900
GTGATTTTGG GGAGCGCGCG GTTCTTCAAC TCGACCAAGT CCGCGCTCTC GGGATTCTTC      960
AACACCGGTC CGGTATAGCG GTCCGCGCTC CTGAACCTCG GTGCGCAACAA TTCTGGCTTC      1020
TTCAACTCTT CGTGGGGGGG CATCGGTAAC TCGGCGCTCG CAAACCGCGG CGTCTCTGTA      1080
TCGGGCGTGA TCAACTCGGG CAACACGTA TCGGCTTTGT TCAACATGAG CCGTGGTGGC      1140
ATCAACACCG CCGGCTTGAT CTGCGGCTTC TTCAACACCG GAAACACAT GTCGGATTTT      1200

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TTGGGTGGCC	CACCGTCTT	CAATCTGGG	CTGGCAACC	GGGGCTGCT	GAACATCTC	1260
GGCAACGCCA	ACATCGGCA	TTCAACATT	CTGGGAGCG	GAACCTGG	TGACTTCAAC	1320
ATCGTTGGCA	GGGCAACCT	GGGAGGCA	AACATCTTG	GCAGGGCA	CTCGGCAAC	1380
TTCAATATCG	GCAGTGA	CATCGGATA	TTCAATGTC	GTTCGGGAG	CTCGGGAAC	1440
TACAACATCG	GATCGGAA	CTCGGGATC	TACAACATCG	GTTCGGAA	CTCGGGGAC	1500
TACAACCTCG	GCTTCGGAA	CGCGGGGAC	TTCAACCAAG	GCTTTGCCAA	CACCGGCAAC	1560
AACAACATCG	GTTTCGGCA	CACCGGCAAC	AACAACATCG	GCATCGGGCT	GTTCGGGAC	1620
AACGAGCAG	GCTTCAATAT	TGCTAGCGG	TGGAACTGG	GCATCGGCA	CAGCGGCTC	1680
TTCAATTCG	GCACCAATA	GCTTGGCATC	TTCAACGCG	GCACGGAA	CTCGGGCATC	1740
GCAAACTCG	GCACGGGAA	CTCGGGATC	GGGAACCGG	GTACCGACAC	TACCGGCATC	1800
CTCAATCTG	GCAGCTACAA	CACCGGCATC	CTCAACGCG	GGGACTTCA	CACGGGCTTC	1860
TACAACAGCG	GCAGCTACAA	CACCGGCGG	TTCAACCTCG	GTAACACAA	CACGGGCAAC	1920
TTCAACCTCG	GTACACCAA	TACCGGCAGC	TATAACCTCG	GTACACCAA	CACGGGCTTC	1980
TTCAATCTCG	GCAACGTCAA	TACCGGCGCT	TTCAACAGCG	GGGACTTCAA	CAATGGCTTC	2040
TTGGTGGCG	GCATTAACCA	GGGCGAGAT	GCATCGATC	TCTCGGTCAC	CATCTCATTC	2100
ATCGGATATA	AGTAGCAGAT	GCTCATTCAC	GTACACCAAG	TAATGACCT	GGCGGCAAC	2160
ATGATCAGCG	TGCTGAGCG	CTGAGGCTT	TTGGGCAAA	GCTTCATAT	GAGCGGTTG	2220
TTCTTTCTCG	GCGCGGTCAA	TCTGAGGCA	TGCAAGCTGA	CGGTTGCGAC	GATCAGCTTC	2280
AGCATCGGCG	CACCGAGCT	GACGCTCGCT	ATCAGCATTC	TCTGTGCTCT	GAGAGGCGG	2340
AGGATTACCT	TCTTCAAGAT	CGATCGGCG	CGCGGCATCG	GAATTTGAG	CACCAACCG	2400
TCTTCGCGCT	TCTTCAACTC	GGGACGCT	GGGACATCG	GCTTCGAA	CGTGGCGGCG	2460
GGCAGTTCAAG	GCTTCGAA	CAGTGGTTG	AGCAGGCGA	TAGGAATTC	GCGTTTCCAG	2520
AACCTCGGCT	GCTTCAGTC	AGGCTGGGCG	AACCTGGGCA	ACTCGGATC	GGGCTTTTT	2580
AACGAGGATA	GCTTGAACCT	CTCGAGCGG	GCAATGCT	CGGCTGGA	CAACATCGG	2640
AGCAAGCTGT	CGGCTGCTT	CGCGGTCG	ACCGGAGCA	TTTTCAGCG	GGGCTTGC	2700
AACCTGGGCT	AGTTGAACAT	CGGAGGCGG	TGCTGCGAA	TTGGGACGA	GTTAGATAG	2760
GTTTCAACAA	TGATATCGG	GTTTTCGCG	AGTGCATCAG	ACGAATCGAA	CGCGGGAAG	2820

GTAAGCGAAT AAACCGAATG GCGGCTGTG AT

2952

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Gly Gln Asn Ala Pro Ala Ile Ala Ala Thr Glu Ala Ala Tyr Asp Gln  
 1 5 10 15  
 Met Trp Ala Gln Asp Val Ala Ala Met Phe Gly Tyr His Ala Gly Ala  
 20 25 30  
 Ser Ala Ala Val Ser Ala Leu Thr Pro Phe Gly Gln Ala Leu Pro Thr  
 35 40 45  
 Val Ala Gly Gly Gly Ala Leu Val Ser Ala Ala Ala Ala Gln Val Thr  
 50 55 60  
 Thr Arg Val Phe Arg Asn Leu Gly Leu Ala Asn Val Arg Glu Gly Asn  
 65 70 75 80  
 Val Arg Asn Gly Asn Val Arg Asn Phe Asn Leu Gly Ser Ala Asn Ile  
 85 90 95  
 Gly Asn Gly Asn Ile Gly Ser Gly Asn Ile Gly Ser Ser Asn Ile Gly  
 100 105 110  
 Phe Gly Asn Val Gly Pro Gly Leu Thr Ala Ala Leu Asn Asn Ile Gly  
 115 120 125  
 Phe Gly Asn Thr Gly Ser Asn Asn Ile Gly Phe Gly Asn Thr Gly Ser  
 130 135 140  
 Asn Asn Ile Gly Phe Gly Asn Thr Gly Asp Gly Asn Arg Gly Ile Gly  
 145 150 155 160  
 Leu Thr Gly Ser Gly Leu Leu Gly Phe Gly Gly Leu Asn Ser Gly Thr  
 165 170 175  
 Gly Asn Ile Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Ile Gly  
 180 185 190  
 Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn Ser Gly Asn Ser Tyr  
 195 200 205  
 Asn Thr Gly Phe Gly Asn Ser Gly Asp Ala Asn Thr Gly Phe Phe Asn  
 210 215 220  
 Ser Gly Ile Ala Asn Thr Gly Val Gly Asn Ala Gly Asn Tyr Asn Thr

225	230	235	240
Gly Ser Tyr Asn Pro Gly Asn Ser Asn Thr Gly Gly Phe Asn Met Gly	245	250	255
Gln Tyr Asn Thr Gly Tyr Leu Asn Ser Gly Asn Tyr Asn Thr Gly Leu	260	265	270
Ala Asn Ser Gly Asn Val Asn Thr Gly Ala Phe Ile Thr Gly Asn Phe	275	280	285
Asn Asn Gly Phe Leu Trp Arg Gly Asp His Gln Gly Leu Ile Phe Gly	290	295	300
Ser Pro Gly Phe Phe Asn Ser Thr Ser Ala Pro Ser Ser Gly Phe Phe	305	310	315
Asn Ser Gly Ala Gly Ser Ala Ser Gly Phe Leu Asn Ser Gly Ala Asn	320	325	330
Asn Ser Gly Phe Phe Asn Ser Ser Ser Asn Gly Ala Ile Gly Asn Ser Gly	335	340	345
Leu Ala Asn Ala Gly Val Leu Val Ser Gly Val Ile Asn Ser Gly Asn	350	355	360
Thr Val Ser Gly Leu Phe Asn Met Ser Leu Val Ala Ile Thr Thr Pro	365	370	375
Ala Leu Ile Ser Gly Phe Phe Asn Thr Gly Ser Asn Met Ser Gly Phe	380	385	390
Phe Gly Gly Pro Pro Val Phe Asn Leu Gly Leu Ala Asn Arg Gly Val	395	400	405
Val Asn Ile Leu Gly Asn Ala Asn Ile Gly Asn Tyr Asn Ile Leu Gly	410	415	420
Ser Gly Asn Val Gly Asp Phe Asn Ile Leu Gly Ser Gly Asn Leu Gly	425	430	435
Ser Gln Asn Ile Leu Gly Ser Gly Asn Val Gly Ser Phe Asn Ile Gly	440	445	450
Ser Gly Asn Ile Gly Val Phe Asn Val Gly Ser Gly Ser Leu Gly Asn	455	460	465
Tyr Asn Ile Gly Ser Gly Asn Leu Gly Ile Tyr Asn Ile Gly Phe Gly	470	475	480
Asn Val Gly Asp Tyr Asn Val Gly Phe Gly Asn Ala Gly Asp Phe Asn	485	490	495
Gln Gly Phe Ala Asn Thr Gly Asn Asn Asn Ile Gly Phe Ala Asn Thr	500	505	510
	515	520	525



Gly Asn Asn Asn Ile Gly Ile Gly Leu Ser Gly Asp Asn Gln Gln Gly  
 530 535 540  
 Phe Asn Ile Ala Ser Gly Trp Asn Ser Gly Thr Gly Asn Ser Gly Leu  
 545 550 555 560  
 Phe Asn Ser Gly Thr Asn Asn Val Gly Ile Phe Asn Ala Gly Thr Gly  
 565 570 575  
 Asn Val Gly Ile Ala Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn  
 580 585 590  
 Pro Gly Thr Asp Asn Thr Gly Ile Leu Asn Ala Gly Ser Tyr Asn Thr  
 595 600 605  
 Gly Ile Leu Asn Ala Gly Asp Phe Asn Thr Gly Phe Tyr Asn Thr Gly  
 610 615 620  
 Ser Tyr Asn Thr Gly Gly Phe Asn Val Gly Asn Thr Asn Thr Gly Asn  
 625 630 635 640  
 Phe Asn Val Gly Asp Thr Asn Thr Gly Ser Tyr Asn Pro Gly Asp Thr  
 645 650 655  
 Asn Thr Gly Phe Phe Asn Pro Gly Asn Val Asn Thr Gly Ala Phe Asp  
 660 665 670  
 Thr Gly Asp Phe Asn Asn Gly Phe Leu Val Ala Gly Asp Asn Gln Gly  
 675 680 685  
 Gln Ile Ala Ile Asp Leu Ser Val Thr Thr Pro Phe Ile Pro Ile Asn  
 690 695 700  
 Glu Gln Met Val Ile Asp Val His Asn Val Met Thr Phe Gly Gly Asn  
 705 710 715 720  
 Met Ile Thr Val Thr Glu Ala Ser Thr Val Phe Pro Gln Thr Phe Tyr  
 725 730 735  
 Leu Ser Gly Leu Phe Phe Phe Gly Pro Val Asn Leu Ser Ala Ser Thr  
 740 745 750  
 Leu Thr Val Pro Thr Ile Thr Leu Thr Ile Gly Gly Pro Thr Val Thr  
 755 760 765  
 Val Pro Ile Ser Ile Val Gly Ala Leu Glu Ser Arg Thr Ile Thr Phe  
 770 775 780  
 Leu Lys Ile Asp Pro Ala Pro Gly Ile Gly Asn Ser Thr Thr Asn Pro  
 785 790 795 800  
 Ser Ser Gly Phe Phe Asn Ser Gly Thr Gly Gly Thr Ser Gly Phe Gln  
 805 810 815

Asn Val Gly Gly Gly Ser Ser Gly Val Trp Asn Ser Gly Leu Ser Ser  
820 825 830

Ala Ile Gly Asn Ser Gly Phe Gln Asn Leu Gly Ser Leu Gln Ser Gly  
835 840 845

Trp Ala Asn Leu Gly Asn Ser Val Ser Gly Phe Phe Asn Thr Ser Thr  
850 855 860

Val Asn Leu Ser Thr Pro Ala Asn Val Ser Gly Leu Asn Asn Ile Gly  
865 870 875 880

Thr Asn Leu Ser Gly Val Phe Arg Gly Pro Thr Gly Thr Ile Phe Asn  
885 890 895

Ala Gly Leu Ala Asn Leu Gly Gln Leu Asn Ile Gly Ser Ala Ser Cys  
900 905 910

Arg Ile Arg His Gln Leu Asp Thr Val Ser Thr Ile Ile Ser Ala Phe  
915 920 925

Cys Gly Ser Ala Ser Asp Gln Ser Asn Pro Gly Ser Val Ser Gln  
930 935 940

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GGATCCATAT GGGCCATCAT CATCATCATC ACCTGATCGA CATCATCGGG ACC

53

## (2) INFORMATION FOR SEQ ID NO:201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CCTGAATTCA GGCTCTGGTT GGGCGGGCCT CATCTTGAC GA

42

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (x1) SEQUENCE DESCRIPTION: SEQ ID NO:202:  
GGATCTGTGCA GGCTGGAAAC CACCGAGCGG T 31
- (2) INFORMATION FOR SEQ ID NO:203:  
(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO:203:  
CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T 31
- (2) INFORMATION FOR SEQ ID NO:204:  
(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO:204:  
GGATCCAGCG CTGAGATGAA GACGATGCC GCT 33
- (2) INFORMATION FOR SEQ ID NO:205:  
(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO:205:  
GGATATCTGC AGAATTCAGG TTAAAGCCC ATTGCGA 38
- (2) INFORMATION FOR SEQ ID NO:206:  
(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO:206:  
CCGATGCGA GCCACGTGCC CACAACGCC 39
- (2) INFORMATION FOR SEQ ID NO:207:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CTTCATGGAA TTCTCAGGCC GTAAGGTCC GCTCCGG 37

(2) INFORMATION FOR SEQ ID NO:208:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7676 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TGGCGAATGG GACGCCCCCT GTAGCGCGCG ATTAAGCGCG GCGGCTGTGG TGGTTACCGG 60  
 CAGCGTGACC GTTACACTTG CCAGCGCCCT AGCGCCCGCT CCTTTGCGTT TCTTCCCTTC 120  
 CTTTCTCGCG AGGTTGCGCG GCTTTCCCGG TCAAGCTCTA AATCGGGGCG TCCCTTTAGG 180  
 GTTCGGATTG AGTGCTTTAC GGCACCTCGA CCCCCAAAAA CTTCATTAGG GTGATGCTTC 240  
 ACCTAGTGGG CCATCGCCCT GATAGACGCT TTTTGGCCCT TTGACGTTGG AGTCCACGTT 300  
 TTTAATAGT GGACTCTGTT TCCAAACTGG AACACACTCG AACCTATCT CGGTCTATTC 360  
 TTTTGATTGA TAAGGATTTC TCGGATTTC GGCCTATTGG TTAAAAATG AGCTGATTTA 420  
 AAAAAATTT AACCGGAATT TTAACAAAT ATTAACGTTT ACAATTTGAG GTGGCACTTT 480  
 TCGGGGAAT GTGCGGGGAA CCGCTATTGG TTTATTTTTC TAAATACATT CAAATATGTA 540  
 TCGGCTCATG AATTATTTCT TAGAAAACT CATCGACCAT CAAATGAAAC TCGAATTTAT 600  
 TCATATCAGG ATTATCAATA CGTATTTTTT GAAAAAGCGG TTCTGTATAT GAAGGAGAAA 660  
 ACTCACCGAG CGAGTTCCAT AGGATGGCAA GATCTGTGTA TCGGTGTGCG ATTCGGCACTC 720  
 GTCCACACTC AATACAACTT ATTAATTTCC CCTCTCAAA AATAAGTTTA TCAAGTGAGA 780  
 AATCACCTGG AGTGACGACT GAATCGGCTG AGAATGGCAA AAGTTTATGC ATTTCTTTCC 840  
 AGACTTTTTC AACAGGCGAG CCATTACCTT COTCATGAAA ATCACTCCCA TCAACCAAAC 900  
 CGTTATTCAT TCGTGATTGC GCCTGAGCGA GACGAAATAG CGGATCCGCT TTAAGAGGAC 960  
 AATTACAAAC AGGAATCGAA TGCACCGGCG GCAGGAACAC TGCCAGCGCA TCAACAATAT 1020  
 TTTCACTTGA ATCAGGATAT TCTTCAATA CTTGGAATGC TTTTTCGCG GGGATCGCAG 1080

TGTTGAGTAA	CCATGCATCA	TCAGGAGTAC	GGATAAAATG	CTTGATGGTC	GGAGAGGGCA	1140
TAAATTCGCT	CAGCCAGTTT	AGTCTGACCA	TCTCATCTGT	AACATCATTT	GCAACGCTAC	1200
CTTTGCCATG	TTTCAGAAAC	AATCTGCGCG	CATCGGGCTT	CCCATACAAAT	CGATAGATTG	1260
TGCGACCTGA	TGCGCCGACA	TTATCGCGAG	CCCATTATATA	CCCATATAAA	TCAGCATCCA	1320
TGTTGGAAAT	TAATCGCGCG	CTAGAGCAAG	ACGTTTCCCG	TTGAATATGG	CTCATAACAC	1380
CCCTTGTAAT	ACTGTTTATG	TAAGCAGACA	GTTTTATTGT	TCATGACCAA	AATCGCTTAA	1440
CGTGAGTTTT	CGTTCCACTG	AGCGTCAGAC	CCCGTAGAAA	AGATCAAAAG	ATCTTCTTGA	1500
GATCCTTTTT	TTCTGCGCGT	AATCTGCTGC	TTGCAAAACAA	AAAAACGACC	GCTACGAGCG	1560
GTGTTTGTGT	TGCGGATCA	AGAGCTACCA	ACTCTTTTTC	CGAAGGTAAAC	TGGTTTCAGC	1620
AGAGCGCAGA	TACCAATAT	TCTCTTCTTA	GTGTAGCGGT	AGTTAGGCCA	CGACTTCAGG	1680
AATCTGTATG	CACCGGCTAC	ATACCTCGCT	CTGCTAATCC	TGTTACCACT	GGGTGCTGCC	1740
AGTGCCGATA	AGTCGTGTCT	TACCGGTTG	GACTCAAGAC	GATAGTTACC	GGATAAGGCG	1800
CAGCGGTGGG	GCTGAACGGG	GGTTCTGTGC	ACACAGCCCA	GCTTGGAGCG	AACGAGCTAC	1860
ACCGAACTGA	GATACCTACA	CGSTGAGCTA	TGAGAAAGCG	CCACCGCTTC	CGAAGGGAGA	1920
AAGCGGACAA	CGTATCGGCT	AAGCGGCGGG	GTCCGAAACAG	GACAGCGCAC	GAGCGAGCTT	1980
CCAGGGGGAA	ACGCGTGGTA	TCTTTATAGT	CGTGTGCGGT	TTCCGCCACT	CTGACTTGAG	2040
CGTCGATTTT	TGTGATGCTC	GTGCGGGGGG	GGGAGCCTAT	GGAAAAACGC	CAGCAACGCC	2100
GCCTTTTATC	GGTTCTGGGC	CTTTTCTGGG	CGTTTTCGTC	ACATGTTCTT	TCTGCGCTTA	2160
TCCCGTGATT	CTGTGGATAA	CGSTATTACC	GCCTTTGAGT	GAGCTGATAC	TCTCTGCGGC	2220
AGCGGAACGA	CGGAGCGCAG	CGATCAGTGC	AGCGAGGAGG	CGGAAGAGCG	CGTGATGCGG	2280
TATTTTCTCC	TTACGCATCT	GTGCGTATTT	TGACACCGCA	TATATGGTGC	ACTCTCAGTA	2340
CGATCTGCTC	TGATGCGCGA	TAGTTAAGCT	AGTATACACT	CCGCTATCGC	TACGTGACTG	2400
GGTCATGGCT	CGCCCCCGAC	ACCGCGCAAC	ACCGCGTGAC	CGCGCCTGAC	GGGCTTGCTT	2460
GTCTCCGGCA	TCCGCTTACA	GACAAGCTGT	GACCGTCTCC	GGGAGCTGCA	TGTGTACAGG	2520
GTCTTCACCG	TCATCACCGA	AACGCGCGAG	GCAGCTCCCG	TAAAGCTCAT	CAGCGTGGTC	2580
GTGAAGCGAT	TCACAGATGT	CTGCGTCTTC	ATCGCGCTCC	AGCTCGTTGA	GTCTCTCCAG	2640
AAGCGTTAAT	GTCTGGCTTC	TGATAAAGCG	GGCGATGTTA	AGGCGGGTTT	TTTCTCTTTT	2700

GCTCACTGAT	GCCTCCGTGT	AAGGGGGAAT	TCTTTTCATG	GGGTAATGA	TACCGATGAA	3760
ACGAGAGAGG	ATGCTCACGA	TACGGGTAC	TGATGATGAA	CATGCCCGGT	TACTGGAAAG	3820
TTGTACGGGT	AAACAACCTGG	CGGTATGGAT	GCGGGCGGAC	CAGAGAAAAA	TCATCCAGGG	3880
TCAATGCCAG	CGCTTCGTTA	ATACAGATGT	AGGTGTTCCA	CAGGGTAGCC	AGCAGCATCC	3940
TGGGATGCAG	ATCCGGAACA	TAATGGTGCA	GCGCGCTGAC	TTCCGCGTTT	CCAGACTTTA	3990
GGAAACACGG	AAACCGAAGA	CCATTCAATG	TGTTGCTCAG	GTCGCAGAGG	TTTTGCAGCA	3960
GCAGTCCGCT	CAAGTTCGGT	CGCTATCGG	TGATTCATTC	TGCTAACCAG	TAAGGCAACC	3120
CGCGCAGCTT	AGCGCGGTGC	TCAACGACAG	GAGCAGGATC	ATCGGCACCC	GTGGGGCGGC	3180
CATGCCGGCG	ATAATGGGCT	GCTTCTCGCC	GAAACGTTTG	GTGGCGGGAC	CAGTGACGAA	3240
GGCTTGAGCG	AGGGCGTGCA	AGATTCCGAA	TACCGCAAGC	GACAGCGCGA	TCATCTGTGC	3300
GCTCCAGCGA	AAGCGTCCCT	CGCGGAAAAA	GACCCAGAGC	GCTCCCGGCA	CGTCTCTAC	3360
GAGTTGCATG	ATAAAGAAGA	CAGTCATAAG	TGCGGCGAGG	ATAGTCATGC	CGCGCGCCCA	3420
CGGGAAGGAG	CTGACTGGGT	TGAAGGCTCT	CAAGGGGATC	GGTGAGAGTC	CGGTGCGCTA	3480
ATGAGTGAGC	TAAGTTACAT	TAATTGCTT	GCGCTCACTG	CGCGCTTTCC	AGTGGGGA	3540
CGTGTCTTGC	CAGCTGCATT	AATGAATCGG	CCAACGCGCG	GGGAGAGCGG	GTTTGCGTAT	3600
TGGCGCCGAG	GCTGCTTTTT	CTTTTCACCA	GTGAGACGGG	CAACAGCTGA	TTGCGCTTCA	3660
CGCGCTGGCC	CTGAGAGAGT	TGCAGCAAGC	GGTCCAGGCT	GGTTTGCCGC	AGCAGCGGAA	3720
AATCGTGTTT	GATGGTGGTT	AACGCGCGGA	TATAACATGA	GCTGTCTTCC	GTATGCTGCT	3780
ATCCCACTAC	CGAGATATCC	GCACCAAGGC	GCAGCCCGGA	CTCGGTAATG	GCGCGCATTC	3840
CGCCGACGCG	CATCTGATCG	TTGGCAACCA	GCATCGAGT	GGGAACGATG	CGCTCATTC	3900
GCATTTGCAAT	GTTTTGTTGA	AAACCGGACA	TGGCACTCCA	GTGCGCTTCC	CGTTCCGCTA	3960
TGCGCTGAAT	TTGATTGCGA	GTGAGATATT	TATGCCAGCC	AGCCAGACGC	AGACGCGCGG	4020
AGACGGAAGT	TATGGGCGCC	GCTAACAGCG	CGATTTCGTC	GTGACCCAT	GCGACCAAGT	4080
GCTCCAGCGC	CAGTCGCGTA	CGCTTTTCAT	GGGAGAAAAA	AATACTGTTG	ATGGGTGTCT	4140
GTTCAGAGAG	ATCAAGAAAA	AACGCGGGA	CATTAGTGCA	GGCAGCTTCC	ACAGCAATGG	4200
CATCTGTGTC	ATCCAGCGGA	TAGTTAATGA	TCAGCCCACT	GACGCGTTCC	GCGAGAGAT	4260
TTGTGACCGG	CGCTTTACAG	GCTTCCAGCG	CGCTTCGTTG	TACCATCGAC	ACGCCACGCG	4320
TGGCACCGAG	TTGATGGCGG	CGAGATTAA	TGCGCGCGAC	AATTTCCGAC	GCGCGTGCA	4380

GGGCCAGACT	GGAGGTGGCA	ACGCCAATCA	GCAACGACTG	TTGGCCCCGC	AGTTGTTTGT	4440
GCACGGGTTT	GGGAATGTAA	TTGAGCTCCG	CCATGGCCGC	TTCCACTTTT	TCCGGGCTTT	4500
TGCGAGAAAC	GTGGCTGGCC	TGGTTACCA	CGCGGAAAC	GGTCTGATAA	GAGACACCGG	4560
CATAGTCTGC	GACATCGTAT	AAGCTTACTG	GTTTCACATT	CACCAACCTG	AATTGACTCT	4620
CTTCGGGGCG	CTATCATGCC	ATACCGCGAA	AGGTTTTCGG	CCATTGCGATG	GTGTCCGGGA	4680
TCTCGAGGCT	CTCCCTTATG	CGACTCTCTG	ATTAGGAAGC	AGCCCGATAG	TAGGTTGAGG	4740
CCGTTGAGCA	CGCCCGCCGC	AAAGAAATGG	GCATGCGAGG	AGATGGCGCC	CAACAGTCCC	4800
CCGGCCACGG	GGCTTCCAC	CATACCCACG	CGAAACAAG	CGCTCATGAG	CCGGAAGTGG	4860
CGAGCCCGAT	TTTCCCATC	GTTGATGTGG	CGGATATAGG	CGCCAGCAAC	CGCACTGTGT	4920
GGCGCGGTGA	TGCGGGCCAC	GATGGGTTCG	GGTAGAGGA	TGGAGATCTC	GATCCCGGGA	4980
AATTAATACG	ACTCACTATA	GGGGAATTGT	GAGCGGATAA	CAATTCCGCT	CTAGAAATAA	5040
TTTTGTTTTA	CTTGAAGAG	GAGATATACA	TATGGGCCAT	CATCATCTTC	ATCACTGTAT	5100
CGACATCTTC	GGGACCGCC	CCACATCTTG	GGAACAGCGG	GGCGCGGAGG	CGGTCCAGCG	5160
GGCGCGGGAT	AGCGTCGATG	ACATCTGGCT	CGCTGGGTC	ATTGAGCAGG	ACATGGCGCT	5220
GGACAGCGCC	GGCAGATCA	CTTACCGCAT	CAAGCTCGAA	GTGTCTTTCA	AGATGAGGCT	5280
GGCGCAACCG	AGGGGCTCGA	AACCAACGAG	CGGTTGGGCT	GAACCGGGCG	CGGGCCCGCG	5340
TACTGTGCGG	ACTAGCGCGG	GTCCTGCGCC	GGTACGTTG	GCGGAGACCG	GTAGCAGGCT	5400
GGCTACCGCG	CTGTTCAACG	TGTGGGGTCC	GGCTTTTCAC	GAGAGGTATC	CGAAGCTCAC	5460
GATCAGCGCT	CAGGCAACCG	GTTCGTGTGC	CGGATCGCG	CAGGCGCGCG	CGGGACGCT	5520
CAACATTGGG	GCTTCGAGCG	GCTATCTGTC	GGAGGTGAT	ATGGCCCGCG	ACAAGGGGCT	5580
GATGACATTC	GGCTAGCGCA	TCTCGGCTCA	CGAGGTCAAC	TACCACTGCG	CGGAGTGAAG	5640
CGAGGACCTC	AAGCTGAACG	GAAGAAGTCT	GGCGGCCATG	TACCAAGCCA	CCATCAAAAC	5700
CTGGGACGAG	CGCGAGATCG	CTGCGCTCAA	CCCCGGCGTG	AACCTGCGCG	GCACCGCGGT	5760
AGTTCCGCTG	CACCGCTCGG	ACGGGTTCGG	TGACACCTTC	TTGTTCAACC	AGTACCTGTC	5820
CAAGCAAGAT	CGCGAGGCTT	GCGGCAAGTC	GCCCCGGCTC	GGCACCACCG	TGACTTCCG	5880
GGCGGTGCGG	GCTGCGCTGG	GTGAGAAACG	CAACGGCGCG	ATGGTGACCG	GTTGCGCGGA	5940
GACACGGGGG	TGGTGGCGCT	ATATCGGCAT	CAGCTTGGTC	GACCAAGCCA	GTCACGCGGG	6000

ACTGCGCGAG	GCCCAACTAG	GCAATAGCTC	TGCAATTTC	TTGTTGCCCC	ACGCCAAG	6060
CATTGAGGCC	GCGCGCGCTG	GCTTGGCAGC	GAAACCCCG	GCGAACCGG	CGATTTCGAT	6120
GATCGACGGG	CGCGCCCCGG	ACGGCTACCC	GATCATCAAC	TACGAGTACG	CGATGCTCAA	6180
CAACCGGCAA	AAGGACGCGG	CGACCGCGCA	GACCTTGCAG	GCATTTCGCG	ACTGCGCGAT	6240
CACCGACGGC	AACAAGCGCT	CGTTGCTCGA	CGAGGTCAT	TTGCGCGCG	TGCGCGCGCG	6300
GCTGCTGAG	TTGTGTGACG	CGTTGATCGC	GACGATTTC	AGCGCTGAGA	TGAGACCGCA	6360
TGCGCTACG	CTCGCGCAGG	AGCGAGTAA	TTTGAGCGG	ATCTCGCGCG	ACCTGAAAG	6420
CGAGATCGAC	CAGGTGGAAT	CGACCGCAGG	TTCTTTGCAG	GCGCAGTGGC	CGCGCGCGCG	6480
GCGGACGGCC	GCCGAGGCGG	CGTGTGTGCG	CTTCGAGAA	GCAGCCAAAT	AGCAGAGCA	6540
GGAAGTCGAC	GAGATCTGCA	CGAATATTGG	TCAGGCGCGC	GTCCAATACT	CGAGGCGCGA	6600
GGAAGGACAG	CAGCAGGCGC	TGTCTCTGCA	AATGGGCTTT	GTGCCCCACA	CGCGCGCGCT	6660
GCGCGCGCTG	ACCGCTGCGC	CGCGACCGCG	ACCGCGGACA	CGTGTGTGCG	CGCGACGACC	6720
GCGCGCGCGG	AACACGCGCA	ATGCCGAGCG	GCGCGATCCC	AACCGAGCAC	CTCGCGCGCG	6780
CGACTCGAAG	GCAACGCGCG	CAGCTGTGAT	TGCGCCAAAC	GCAACCGCAC	CTGTGCGGAT	6840
CGACAACTCG	GTGCGAGGAT	TCAGCTTTCG	GTGCGCTGCT	GCTGCGGTGG	AGTCTGACGC	6900
CGCGCACTTC	GACTAGCGGT	CAGCATCTCT	CAGCAAAAGC	ACCGGCGGAG	CGCGATTTCC	6960
CGGACAGCGG	CGCGCGGTGG	CGAATGACAC	CGGTATCTTG	CTCGCGCGCG	TAGAGCAAAA	7020
GCTTTAGCGC	AGCGCGGAG	CGACCGAGTC	CAAGCGCGCG	GCGCGGTGG	GCTGCGGAT	7080
GCGTGAGTTC	TATATGCGCT	ACCGCGGCGC	CGCGATCAAC	CAGGAAACCG	TCTCGCTTGA	7140
CGCGCAACCG	GTGCTGAGAA	CGCGCTCGTA	TTACGAAATC	AAGTTCAGCG	ATCGGAGTAA	7200
GCGGACGCGC	CAGATCTGGA	CGCGCTTAAT	CGGCTCGCGC	GCGCGGAGCG	CACCGGAGCG	7260
GCGCGCGCGT	CAGCGCTGCT	TTGTGCTATG	GCTCGGAGCG	GCCAACAACC	CGGTGAGCAA	7320
GCGCGCGCGC	AAGGCGCTGG	CGGAATCGAT	CGCGCGCTTG	GTGCGCGCGC	CGCGCGCGCG	7380
GCGCAGCGCT	CGTGCAGAGC	CGGCTCGCGC	GCGCGCGCGC	GCGCGGAGAG	TGCGCTCTAC	7440
GCGGACGACA	CGGACACGCG	AGCGGACCTT	ACCGCGCTGA	GAACTCTGCA	GATATGCTAT	7500
AGACTGCGCG	CGGCTCGAGC	ACCAACACCA	CGACCACTGA	GATCGCGCTG	CTAACAAAGC	7560
CGGAAAGGAA	GCTGAGTTGG	CTGCTGCCAC	CGCTGAGCAA	TAACTAGCAT	AACCGCTTGG	7620
GCGCTCTTAA	CGGCTCTTGA	GCGGTTTTTT	GCTGAAAGGA	GGAATATAT	CGCGAT	7676



## (2) INFORMATION FOR SEQ ID NO:209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

Met Gly His His His His His Val Ile Asp Ile Ile Gly Thr Ser
 1              5              10              15

Pro Thr Ser Trp Gln Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
20              25              30

Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
35              40              45

Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Gln Val
50              55              60

Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser
65              70              75              80

Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro
85              90              95

Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr
100             105             110

Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn
115             120             125

Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln
130             135             140

Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser
145             150             155             160

Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala
165             170             175

Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His
180             185             190

Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile
195             200             205

Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn
210             215             220

Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly
225             230             235             240

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Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly  
 245 250 255  
 Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val  
 260 265 270  
 Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys  
 275 280 285  
 Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp  
 290 295 300  
 Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser  
 305 310 315 320  
 Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala  
 325 330 335  
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp  
 340 345 350  
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile  
 355 360 365  
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala  
 370 375 380  
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp  
 385 390 395 400  
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp  
 405 410 415  
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala  
 420 425 430  
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu  
 435 440 445  
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly  
 450 455 460  
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg  
 465 470 475 480  
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser  
 485 490 495  
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu  
 500 505 510  
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala  
 515 520 525

Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro  
 530 535 540  
 Val Ala Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro  
 545 550 555 560  
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro  
 565 570 575  
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn  
 580 585 590  
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser  
 595 600 605  
 Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Ser Lys Thr Thr  
 610 615 620  
 Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr  
 625 630 635 640  
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu  
 645 650 655  
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu  
 660 665 670  
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser  
 675 680 685  
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys  
 690 695 700  
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile  
 705 710 715 720  
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp  
 725 730 735  
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala  
 740 745 750  
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro  
 755 760 765  
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala  
 770 775 780  
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu  
 785 790 795 800  
 Pro Ala

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GTGGCGGCGC	TGCGGCGCGC	CAGCAGAGCG	ATGTGCATCC	GTTCGCGAAC	GTGATCGCGC	60
TCGAGCATGA	CGCGCGCGAA	CGCGCGCGAG	ACGAAGAACG	TCAGGAAGCC	GTCCAGCAGC	120
CGCGGTGCGG	CGGTGACGAA	GCTGACCGCG	TGCGAGATCA	GCACGACCGC	GGCGATGCGC	180
CGGACCAATG	TGACCGCGGT	GATCGCGCGC	ACGATCGCGA	CCACGACCGC	CACGAGGAGC	240
ACACCGCAGC	CGCGCGCGGT	GAACCGCGAG	CGGAATCGGT	TGTGACGAA	GATGGCGTCC	300
CGGATCGCGA	TGACGTGCGT	ACCGACCGCG	GGGTGAACCA	CCAGGCGGTA	CGCGGCGTTC	360
TCTTCACCGC	CATGGTTGTT	CAGCAGCTGC	CAGGCGTGGC	GGTGGGTAAT	GCTTCTGCTC	420
GAAGATGAGG	GTGCGCGCAT	CGGTACCGCA	GGCC			454

## (2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

TGCAGAGATG	CGCGCGATCC	TGCGTGGCGC	ACGCGGAACG	GATTCGCGCG	GTGCGCGAAC	60
GCATCGTCGC	CACCAAGAA	CGAGCGATG	ACGTGCTGCT	CGTGTCTCTT	GGCATGGGCG	120
ATAGCACCGA	CGACCTGCTG	GATCTGGCTC	AGCAGGTGTG	CGCGGCGCGC	CGCGCTCGGG	180
AGCTGACATC	GCTGCTTACC	CGCGGTGAAC	GCATCTCGAA	TGCGTTGGTG	GGCATGGGCG	240
TGAGTCTGCT	CGCGCGCATC	CGCGGCTGCT	TCACCGGCTC	GCAGGCGCGG	GTGATCACCA	300
CGCGGACCGA	CGGCAACGCT	AAGATCATCG	ACGTCAACGC	GGGCGGCGTG	CAAAACCGCC	360
TTGAGGAAGG	CGCGGTGCTC	TTGGTGCGCG	GATTCGAAGG	GCTCAGCGAG	GACACCAAGG	420
ATGTCAACAC	GTGCGGCGCG	GGCGGCTCGG	ACACCAACGC	CGTGCCTATG		470

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GGCGGCGGTA	CGCGGCGCGG	ACAAACAACG	ATCGATTGAT	ATCGATGAGA	GACGAGGAGG	60
TGCTGGCGCT	TGCGCATGTC	ACCGACGAGC	AGCGCGCGCG	CGCGTTGGAG	AAGGCTGCTG	120
CGGACGCTCG	AGCGGAGGCA	GAGCTCAAGG	ATCGGCTCAA	CGCTGGCGCG	ACCACTCTCA	180

CCCAGTCTCT	CAAGGACGCG	GAGAGCGATG	AAGTCTGGG	CAAAATGAAG	GTGTCTGGC	240
TGCTTGAGGC	CTTGCCAAAG	GTGGCAAGG	TCCAGGCGC			279

## (2) INFORMATION FOR SEQ ID NO:213:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACACGCTCGA	ACTCGACGAG	CCCTCTGCTG	AGGTGTCGAC	CGACAAGGTC	GACACCGAAA	60
TCCCTGCGCG	CGCGCGGGTG	TGCTGACCAA	GATCATCGCC	CAAGAAGATG	ACACGGTGGG	120
GGTCGGCGGG	GAGCTCTCTG	TCATTGGCGA	CGCCCATGAT	CGCGGCGAGG	CGCGGCTCCC	180
GGCACGCCAG	AAAGTCTCTG	CGGCGCCAAC	CCGAATCCA			219

## (2) INFORMATION FOR SEQ ID NO:214:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:214:

TGCTGCGGA	CATCGCGGCC	GGCGCGGCTT	CGAAGCGGCG	ACCGAAGGCC	GTCCCGGAGC	60
CAGCGCGCGG	GCCGAAGGCC	GAACCGGCGC	CATCGCGGCC	GGCGCGGCGG	CGAGCGGCTG	120
CGGCGCGGAG	CGCAGCGTAC	GTGACGCGCC	TGCTGCGAAA	GCTGCGGCTC	GAAGACAACA	180
TGACCTGCGC	CGGGTGAGCT	GGCAGCGGAG	TGGGTGGTCT	CATCGCGCAA	CAGGATGTGC	240
TGGCGCGCGG	TGACCAAAAG	AAGCGGCGGA	AAGCAGCGGC	GC CGCGCGGC	CGGCGCGCGG	300
CGGCGCGCGG	CGCGAAAGCG	CGGCTGAAG	ATCGATGCGC	GC		342

## (2) INFORMATION FOR SEQ ID NO:215:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GGTCTTGGT	CAGTATCAGC	GGCGACGAGG	AGGCCAGGCT	GGCCCTCGGC	GGCGAGTTGG	60
CGCGGATCGG	TGTGCTCTGC	GACATCGGGG	CGCGCGCGGC	CGCCAGGCCC	GCAGCCAAAGC	120
CGTCCCCCGA	CGCAGCGCGG	ACGCGGAGGG	CGGAACCGGC	ACCATCGCGG	CGCGCGGCGC	180
AGCCAGCGGG	TGCGGCGGAG	GGCGACCGGT	ACGTGACGCC	GCTGCTGCGA	AAGCTGGCGT	240

CGGAAACAA	CATCGACCTC	GGGGGGGTGA	CCGGCACTGG	AGTGGGTGGT	CGCATCCGCA	300
AACAGGATGT	GCTGGCCGCG	GCTGAACAAA	AGAAGCGGGC	GAAAGCACCG	GGGCCCTGAG	360
CGCTTCATCA	CGGGTTTAAC	CAGCTTGCCC	CAGAAGCCGG	CTTCGACCTC	TTGGCGGGTC	420
TTGGTCCGCT	GCAGGGCGTC	GGCGAGCCAG	TTCAAGTTAG	GGGGCCGAAA	TCTTCAGATT	480
CGCCAGGAAG	GGCACCCCGA	ACAGGGTCCG	CAGCC			515

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CGAGCCGCA	GGTCAGATT	CACACGGCCA	TTGAGGAAGC	ACAGCCGACC	CACCAAGCCG	60
TGACTCACA	GGCGCCGCA	GTGATCGGTA	ACCAGCTCTA	ATTGGAGATG	CGACTCAACC	120
GACAGCTGCG	GGACATCGAA	AAGCTTCAGG	TCAATGTGCG	CCAAGCCCTG	ACGCTGGCCG	180
ACCAGGCTAC	CGCGCCCGGA	GACGCTGCGA	AGGCCACCGA	ATACAAACAAC	CCCGCCGAGG	240
CGTTCCGACG	CGAGCTGGTG	ACCGCCGAGC	AGAGCGTCGA	AGAGCTCAAG	ACGCTGCATG	300
ACCAGGCGCT	TAGCGCCGCA	GCTCAGGCCA	AGAAAGCCGT	CGAACGAAAT	CGGATGTTGC	360
TCCAGCCAGAA	GATCCCGGAG	CGAACCAAGC	TGCTCAGCCA	GCTCGAGCAG	CGGAAGATGC	420
AGGAGCAGGT	CAGCGCATCG	TTGCGCTCGA	TGAATGAGCT	GGCGGCGCCA	GGCAACACGC	480
CGAGCTTCGA	CGAGATTGCG	GACAAAGATG	AGCGTCCCTA	CGCCAAAGCG	ATCGGTTCCG	540
CTGAACCTGC	CGAGAGT					557

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CAGGATAGGT	TTGACATCC	ACCTGGGTTG	CGCACCGCGT	GGCGGACCGT	GTGATAGGCC	60
AGAGGTGGAC	CTGGCGCGAC	CGACGATCGA	TGAGGAGTTC	AACAGAAATG	GGCTTCTCGG	120
TCCAGATGCC	GGCACTCGGT	GAGAGCGTCA	CCGAGGGGAC	GCTTACCCCG	TGGCTCAAACT	180
AGGAGGCGGA	CACGCTCGAA	CTGACGAGCG	CCCTGCTGGA	GAT		223

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:218:

AAGAAGTACA	TCTCCGGTTC	GATGTCCGGC	AACCACGGCA	GCCACCGGGC	GCAGTAGCCG	60
ACCAGGACCA	CCGCATAACG	CCAGTCCCGG	CGCACAAACA	TACGCCACCC	CGGATATGCT	120
AGGACTTGCA	CGGCCAGCCA	CCACATCGCG	GGCTGCCGGA	CCAGCATCTC	GGCCTTGACG	180
CACGACTGTG	CGCCGGCAGC	TGCAACGTCT	TGCTGGTCSA	TGGCGTACAG	CACCGGCGCG	240
AACGACATGG	GCCAGGTCCA	CGGTTTGGAT	TGCCAAGGGT	GGTAGTTGCC	TGCGGAATTC	300
GTCAGGCCCG	CGTGGAAAGT	GAACGCTTTG	CGGTTGTATT	GCCAGAGCGA	CGCGACCGCG	360
TCCGGCAGCG	GAACAACCGA	GTTGCGACCG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	420
GGGCTCTCGG	ACGCGAACCA	CGGAGCGTAG	GTGGCCAGAT	AGACCGCGAA	CGGGATCAAC	480
CCACGCGCAT	ACCGCTGGGG	AAGCACGTCA	CGCCGCACGT	TTCCAGGCGA	CGGTCTTTGC	540
ACTTGGTATG	AACGTGCGCG	CGCCACGTCA	ACGCCAGC			578

## (2) INFORMATION FOR SEQ ID NO:219:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:219:

ACAAGCATCG	ATTGATATCG	ATGAGAGACG	GAGGAATCGT	GGCCCTTCCC	CAGTTGACCG	60
ACGAGCAGCG	CGCGGCCCGC	TTGGAGAAAG	GTGCTGCCCG	ACGTCGAGCG	CGAGCAGAGC	120
TCAAGGATCG	GCTCAAGCGT	GGCGGCACCA	ACCTCACCCA	GCTCTTCAAG	GACGCGGAGA	180
GCGATGAAGT	CTTGGGCAAA	ATGAAGTGTG	CTGCGCTGCT	TGAGGGCTTG	CCAAAGGTGG	240
GCAAGGTCAA	GGCCGAGGAG	ATCATGACCG	AGCTGGAAAT	TGCGCCCTCAC	CCGCGCGCGT	300
TGCTGGGCTC	GGTGACGCTC	AGCGCAAGGC	CCTGCTGGAA	AACTTGGGCT	CGGCTTAACC	360
CGGCGCGCGC	ACGATCGCGG	CGGGAAGGCC	TGTGGTGGGC	GTACCCCTCGC	ATACGGGGGA	420
GAAGCGGCGT	GACAGGGCGA	GTTTACAATT	CAGGCGGAAC	CGCCCGGTGG	GGGGGAACCC	480
GCCT						484

## (2) INFORMATION FOR SEQ ID NO:220:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:220:

AGGACTTGCA	CGGCCAGCCA	CCACATCGCG	GGCTGCCGGA	CCAGCATCTC	GGCCTTGACG	60
CACGACTGTG	CGCCGACGCC	TGCAACGTCT	TGCTGGTCSA	TGGCGTACAG	CACCGGCGCG	120
AACGACATGG	GCCAGGTCCA	CGGTTTGGAT	TGCCAAGGGT	GGTAGTTGCC	TGCGGAATTC	180
GTCAGGCCCG	CGTGGAAAGT	GAACGCTTTG	CGGTTGTATT	GCCAGAGCGA	CGCGACCGCG	240
TCCGGCAGCG	GAACAACCGA	GTTGCGACCG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	300
GGGCTCTCGG	ACGCGAACCA	CGGAGCGTAG	GTGGCCAGAT	AGACCGCGAA	CGGGATCAAC	360
CCACGCGCAT	ACCGCTGGGG	AAGCACGTCA	CGCCGCACGT	TCCCGAGCGA	CGGTCTTTGC	420

ACTTGGTACT GACGTCCGCC GCCCACGTCC AACGCCAGCC CCATCGCGCC GAAGAACAGC 480  
ACGAAGTACA CGCCGACCA CTTGGTGGCC CAAGCCATC CCAAGCAGCA CCCCCG 517

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Gly Gly Ala Ala Gly Gln Gln Ser Asp Val His Pro Phe Ala Asn  
1 5 10 15  
Leu Ile Ala Val Asp Asp Glu Arg Ala Glu Arg Arg Asp Asp Glu Glu  
20 25 30  
Arg Gln Glu Ala Val Gln Gln Arg Gly Pro Arg Gly Asp Glu Ala Asp  
35 40 45  
Pro Val Ala Asp Gln Gln His Pro Gly Asp Gly Ala Asp Gln Cys Arg  
50 55 60  
Pro Ala Asp Pro Pro His Asp Pro His His Gln Arg His Gln Asp His  
65 70 75 80  
Thr Gln Gln Gly Ala Gly Glu Pro Pro Ala Glu Ser Val Val Thr Glu  
85 90 95  
Asp Gly Leu Pro Asp Arg Asp Gln Leu Leu Thr Asp Arg Arg Val Asn  
100 105 110  
His Gln Ala Val Pro Gly Val Val Phe His Pro Met Val Val Gln His  
115 120 125  
Leu Pro Gly Leu Ala Val Arg  
130 135

## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Gln Lys Tyr Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg  
1 5 10 15  
Val Ala Glu Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val  
20 25 30  
Val Val Val Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu  
35 40 45  
Ala Gln Gln Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu  
50 55 60  
Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile



65		70		75		80
Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly						
	85		90		95	
Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr						
	100		105		110	
Pro Gly Arg Leu Gln Thr Ala Leu Gln Glu Gly Arg Val Val Leu Val						
	115		120		125	
Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu						
	130		135		140	
Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Met						
145	150		155			

## (2) INFORMATION FOR SEQ ID NO:223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Pro Ala Tyr Pro Ala Gly Thr Asn Asn Asp Arg Leu Ile Ser Met Arg						
1	5		10		15	
Asp Gly Gly Ile Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Ala						
	20		25		30	
Ala Ala Leu Glu Lys Ala Ala Ala Ala Arg Arg Ala Arg Ala Glu Leu						
	35		40		45	
Lys Asp Arg Leu Lys Arg Gly Gly Thr Asn Leu Thr Gln Val Leu Lys						
	50		55		60	
Asp Ala Glu Ser Asp Glu Val Leu Gly Lys Met Lys Val Ser Ala Leu						
	65		70		75	
Leu Glu Ala Leu Pro Lys Val Gly Lys Val Gln Ala						
	80		85		90	

## (2) INFORMATION FOR SEQ ID NO:224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Thr Val Glu Leu Asp Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val						
1	5		10		15	
Asp Thr Glu Ile Pro Ser Pro Ala Ala Gly Val Leu Thr Lys Ile Ile						
	20		25		30	
Ala Gln Glu Asp Asp Thr Val Glu Val Gly Gly Glu Leu Ser Val Ile						
	35		40		45	

Gly Asp Ala His Asp Ala Gly Glu Ala Ala Val Pro Ala Pro Gln Lys  
 50 55 60  
 Val Ser Ala Gly Pro Thr Arg Ile  
 65 70

## (2) INFORMATION FOR SEQ ID NO:225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Ala Ala Asp Ile Gly Ala Ala Pro Ala Pro Lys Pro Ala Pro Lys Pro  
 1 5 10 15  
 Val Pro Glu Pro Ala Pro Thr Pro Lys Ala Glu Pro Ala Pro Ser Pro  
 20 25 30  
 Pro Ala Ala Gln Pro Ala Gly Ala Ala Glu Gly Ala Pro Tyr Val Thr  
 35 40 45  
 Pro Leu Val Arg Lys Leu Ala Ser Glu Asn Asn Ile Asp Leu Ala Gly  
 50 55 60  
 Val Thr Gly Thr Gly Val Gly Gly Arg Ile Arg Lys Gln Asp Val Leu  
 65 70 75 80  
 Ala Ala Ala Glu Gln Lys Lys Arg Ala Lys Ala Pro Ala Pro Ala Ala  
 85 90 95  
 Gln Ala Ala Ala Ala Pro Ala Pro Lys Ala Pro Pro Glu Asp Pro Met  
 100 105 110  
 Pro

## (2) INFORMATION FOR SEQ ID NO:226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala Thr Val Pro Val Gly  
 1 5 10 15  
 Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Asp Ile Gly Ala Ala Pro  
 20 25 30  
 Ala Pro Lys Pro Ala Pro Lys Pro Val Pro Glu Pro Ala Pro Thr Pro  
 35 40 45  
 Lys Ala Glu Pro Ala Pro Ser Pro Pro Ala Ala Gln Pro Ala Gly Ala  
 50 55 60  
 Ala Glu Gly Ala Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Ser

68		70		75		80
Glu	Asn	Asn	Ile	Asp	Leu	Ala
		85		90		95
Arg	Ile	Arg	Lys	Gln	Asp	Val
		100		105		110
Ala	Lys	Ala	Pro	Ala	Pro	
		115				

## (2) INFORMATION FOR SEQ ID NO:227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Asp	Pro	Lys	Val	Gln	Ile	Gln	Gln	Ala	Ile	Glu	Glu	Ala	Gln	Arg	Thr
1			5					10						15	
His	Gln	Ala	Leu	Thr	Gln	Gln	Ala	Ala	Gln	Val	Ile	Gly	Asn	Gln	Arg
			20					25						30	
Gln	Leu	Glu	Met	Arg	Leu	Asn	Arg	Gln	Leu	Ala	Asp	Ile	Gln	Lys	Leu
			35					40					45		
Gln	Val	Asn	Val	Arg	Gln	Ala	Leu	Thr	Leu	Ala	Asp	Gln	Ala	Thr	Ala
			50			55					60				
Ala	Gly	Asp	Ala	Ala	Lys	Ala	Thr	Glu	Tyr	Asn	Asn	Ala	Ala	Glu	Ala
			65			70				75				80	
Phe	Ala	Ala	Gln	Leu	Val	Thr	Ala	Glu	Gln	Ser	Val	Glu	Asp	Leu	Lys
			85					90						95	
Thr	Leu	His	Asp	Gln	Ala	Leu	Ser	Ala	Ala	Gln	Ala	Lys	Lys	Ala	
			100					105						110	
Val	Glu	Arg	Asn	Ala	Met	Val	Leu	Gln	Gln	Lys	Ile	Ala	Glu	Arg	Thr
			115					120						125	
Lys	Leu	Leu	Ser	Gln	Leu	Glu	Gln	Ala	Lys	Met	Gln	Glu	Gln	Val	Ser
			130					135						140	
Ala	Ser	Leu	Arg	Ser	Met	Ser	Glu	Leu	Ala	Ala	Pro	Gly	Asn	Thr	Pro
			145			150				155				160	
Ser	Leu	Asp	Glu	Val	Arg	Asp	Lys	Ile	Glu	Arg	Arg	Tyr	Ala	Asn	Ala
			165					170						175	
Ile	Gly	Ser	Ala	Glu	Leu	Ala	Glu	Ser							
			180					185							

## (2) INFORMATION FOR SEQ ID NO:228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Val Ser Thr Ser Thr Trp Val Pro His Pro Val Arg Asp Arg Val Ile
 1           5           10           15
Gly Gln Arg Trp Thr Cys Ala Asp Arg Arg Ser Ile Glu Glu Ser Thr
          20           25           30
Glu Met Ala Phe Ser Val Gln Met Pro Ala Leu Gly Glu Ser Val Thr
 35           40           45
Glu Gly Thr Val Thr Arg Trp Leu Lys Gln Glu Gly Asp Thr Val Glu
 50           55           60
Leu Asp Glu Pro Leu Val Glu
 65           70

```

## (2) INFORMATION FOR SEQ ID NO:229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Glu Val His Leu Pro Val Asp Val Gly Glu Pro Arg Gln Pro Thr Gly
 1           5           10           15
Ala Val Ala Asp Gln Asp His Arg Ile Thr Pro Val Pro Ala His Lys
          20           25           30
His Thr Pro Pro Arg Val Cys Gln Asp Trp His Arg Gln Pro Pro His
 35           40           45
Arg Gly Arg Ala Asp Gln His Leu Gly Leu Asp Ala Arg Leu Cys Ala
 50           55           60
Ala Ala Cys Asn Val Leu Leu Val Asp Gly Val Glu His Arg Pro Gln
 65           70           75           80
Arg His Gly Pro Gly Pro Arg Phe Gly Phe Pro Arg Val Val Val Ala
          85           90           95
Cys Gly Ile Arg Gln Ala Arg Val Glu Val Glu Arg Phe Gly Gly Val
          100          105          110
Leu Pro Glu Arg Ala His Gly Val Gly Gln Arg Asn Asn Arg Val Ala
          115          120          125
Thr Asp Arg Leu Thr Asp Arg Met Pro Ile Asp Arg Gly Leu Gly Arg
          130          135          140
Glu Pro Arg Ser Val Gly Gly Gln Ile Asp Arg Glu Arg Asp Gln Pro
          145          150          155          160
Gln Arg Ile Pro Ala Gly Lys His Val Thr Pro His Cys Ser Gln Pro
          165          170          175
Arg Ser Leu His Leu Val
          180

```

## (2) INFORMATION FOR SEQ ID NO:230:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

Asn Asp Arg Leu Ile Ser Met Arg Asp Gly Gly Ile Val Ala Leu Pro
 1           5           10           15
Gln Leu Thr Asp Glu Gln Arg Ala Ala Leu Glu Lys Ala Ala Ala
 20           25           30
Ala Arg Arg Ala Arg Ala Glu Leu Lys Asp Arg Leu Lys Arg Gly Gly
 35           40           45
Thr Asn Leu Thr Gln Val Leu Lys Asp Ala Glu Ser Asp Glu Val Leu
 50           55           60
Gly Lys Met Lys Val Ser Ala Leu Leu Gln Ala Leu Pro Lys Val Gly
 65           70           75           80
Lys Val Lys Ala Gln Glu Ile Met Thr Glu Leu Glu Ile Ala Pro His
 85           90           95
Pro Ala Ala Phe Val Ala Ser Val Thr Val Ser Ala Arg Pro Cys Trp
100           105           110
Lys Ser Ser Ala Pro Pro Asn Pro Ala Gly Arg Arg Cys Gly Pro Glu
115           120           125
Gly Leu Trp Trp Ala Tyr Pro Arg Ile Arg Gly Arg Ser Gly Leu Thr
130           135           140
Gly Pro Ala His Asn Ser Gly Arg Thr Pro Arg Trp Gly Gly Thr Arg
145           150           155           160

```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

Asp Trp His Arg Gln Pro Pro His Arg Gly Arg Ala Asp Gln His Leu
 1           5           10           15
Gly Leu Asp Ala Arg Leu Cys Ala Ala Ala Cys Asn Val Leu Leu Val
 20           25           30
Asp Gly Val Gln His Arg Pro Gln Arg His Gly Pro Gly Pro Arg Phe
 35           40           45
Gly Phe Pro Arg Val Val Val Ala Cys Gly Ile Arg Gln Ala Arg Val
 50           55           60
Glu Val Glu Arg Phe Gly Gly Val Val Pro Glu Arg Ala His Gly Val
 65           70           75           80
Gly Gln Arg Asn Asn Arg Val Ala Thr Asp Arg Leu Thr Asp Arg Met
 85           90           95
Pro Ile Asp Arg Gly Leu Gly Arg Glu Pro Arg Ser Val Gly Gln Gly
100           105           110
Ile Asp Arg Glu Arg Asp Gln Pro Gln Arg Ile Pro Ala Gly Lys His

```

	115		120		125
Val	Thr	Pro	His	Cys	Pro
	130		135		140
Ser	Arg	Arg	His	Val	Glu
145			150		155
Glu	Val	His	Ala	Gly	Pro
			165		170
Pro	Arg				175

## (2) INFORMATION FOR SEQ ID NO:232:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

ATGCCAAGCC	GGTGCTGATG	CCCGAGCTCG	CGGAATCGGT	GACCGAGGGG	ACCGTCATTC	60
GTGGCTGAA	GAGGATCGGG	GATTGGGTTC	AGGTTGACGA	GCCACTCGTG	GAGGTGTCCA	120
CGGACAAGST	GGACACCGAG	ATCCCGTCCC	CGGTGGCTGG	GGTCTTGCTC	AGTATCAGCG	180
CGGAGMAGGA	CGGACCGGTS	CGCGTGGCGG	CGGAGTTGGC	CGGGATCGGT	GTGCTGCGCC	240
AGATCGGGCC	GCGCGCGGCC	CCCAAGCCCC	C			271

## (2) INFORMATION FOR SEQ ID NO:233:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: protein

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Ala	Lys	Pro	Val	Leu	Met	Pro	Glu	Leu	Gly	Glu	Ser	Val	Thr	Glu	Gly
1			5				10				15				
Thr	Val	Ile	Arg	Trp	Leu	Lys	Lys	Ile	Gly	Asp	Ser	Val	Gln	Val	Asp
	20					25				30					
Glu	Pro	Leu	Val	Glu	Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile	Pro
	35					40				45					
Ser	Pro	Val	Ala	Gly	Val	Leu	Val	Ser	Ile	Ser	Ala	Asp	Glu	Asp	Ala
	50				55			60							
Thr	Val	Pro	Val	Gly	Gly	Gln	Leu	Ala	Arg	Ile	Gly	Val	Ala	Ala	Glu
65				70				75							80
Ile	Gly	Ala	Ala	Pro	Ala	Pro	Lys	Pro							
							85								

## (2) INFORMATION FOR SEQ ID NO:234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAGGTAGCGG ATGCGCCGAG GAGCACCCCA GGACCGCGCC CGAACCCCGG GTGCGCGTCA 60  
 TCGATATGTG GGCACCGTTC GTTCGCTCCG CCGAGGTGAT TGACGAT 107

## (2) INFORMATION FOR SEQ ID NO:235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

ATGAATGTGA AATTGCTGG CCGAGTACT GCGATACTGG GTTGTGCAGC GCGGTTGTG 60  
 TTCTGTGCTT CGGTGCGGAG CCGGATCCA CCGACCCGCG ATCAGCCCGA CATGACGAAA 120  
 GCGTATTGCC CCGGTGGCGG ATGGGGTTTT GCGGACTTGG CCGTGTCCGA CCGGAGAGAAG 180  
 TACCGGACCG GCTCGTTTTC GCACCACTGG ATGCRAACCT GGTTTACCGG CCGACAGTTT 240  
 TACTTCGATT GTGTACCGCG CGGTGAGCCC CTCCCGGCGC GCGCGCCACC GGGTGTGTTC 300  
 GGTGGGGGAA TTGCTCCGA GCGGCCCAAC GCTGCTGTA 339

## (2) INFORMATION FOR SEQ ID NO:236:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala  
 1 5 10 15  
 Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp  
 20 25 30  
 Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp  
 35 40 45  
 Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly  
 50 55 60  
 Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe  
 65 70 75 80  
 Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro

85	90	95
Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro		
100	105	110

## (2) INFORMATION FOR SEQ ID NO:237:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA

## (X1) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GTGACCACGG	TGGCGCTGCC	ACCAACGCGG	GCAGCGGCGG	CCGCGCGCGG	CCCGCGCGCT	85
CGCGCGCGCA	CGGTGCGGCC	CGGGGTAAAG	CCACCGGCTC	AGCGCGCAAG	CGCGCGCGCG	120
GTGCGCAATG	CGGTGATGGG	AGCTTCGCGG	CTACCGAGCG	CCCGCGCTCC	ATCGGGGTCA	180
CGCGCGCGCG	CGCGCGCAAC	CGCGCGCAAG	CGCGCGCGCG	TGGCAGCAAG	CCCAACGGCT	240
CAGGTGCGCA	CGCGCGCAAA	GGCGCGCAAG	CGCGTGCCTG	CGGCAACCGG	CGCTCGATCG	300
CGCGCAACAG	CGCGATCGTC	CGCGGTTCGG	GTGCGGCGCG	TGGCGCTCGC	CGCGCGCGCG	360
GAAACGCGAG	C					371

## (2) INFORMATION FOR SEQ ID NO:238:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

## (11) MOLECULE TYPE: cDNA

## (X1) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GTGCGGCTCC	CACCAACCGG	CGCGCGCGCG	CGTAGCGCGC	GGGCGCACCA	CGCGCTTTTC	60
TGACTCGGTT	CAAGAAAAGG	CGCTTCGTGT	TGGTCGCGCA	TGTTGGCGATG	ATCGTGACCC	120
ATGGGCAACA	TGCACGTGCA	CATCTCGGCC	AAGGTCTAGC	TGCATGCGAA	TGCGCGCGCG	180
GGTGGTGAGC	ATCGGTCTAG	CGCTCATAGG	AGGCTTCGCG	GTACTCTTTG	CGGACGACAA	240
CGCGTCGCGG	CGCGGGGTTG	TGTCTACGCG	GGTCTCGGGA	AAGGGGTGCG	TGGCAACATC	300
CTCGCGCGCG	CCAATGGGCT	GGGAGCGCGT	GTTCACCAAG	CGTTTCAGGG	CGTTTGGGCT	360
CGAATCATCC	CGGTGCAACA	ACTGGGTGGA	CATCGGCTG	CGGAGGTGT	ACGACGATCC	420
CGAC						424

## (2) INFORMATION FOR SEQ ID NO:239:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA



## (X1) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GCGATGGCGG	CGCGGGGTAC	CACCGCCAAT	GTGGGAACGGT	TTCCCAACCC	CAACGATCCT	60
TTGCATCTGG	CGTCAATTGA	CTTCAGCCCG	GCCGATTTCG	TCACCGAGGG	CCACGCTCTA	120
AGCGCGGATG	CGATCCTACT	CGCGCTTACC	GACCGGCTGC	GTTCGCGCGA	GCGCGCGGAT	180
TGGGACTTGG	TGGAGTTCGA	GTTCGCGACG	ACCGTCACCG	CGGACACGGT	GCGCATCGAC	240
GTCACTCGCG	ACGATATCGG	TCCCGAAGTG	GCGCGCGCGT	CGAACTTCAC	CGAATCGCTG	300
CGGCTCTACG	ATTCTCTC					317

## (2) INFORMATION FOR SEQ ID NO:240:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA

## (X1) SEQUENCE DESCRIPTION: SEQ ID NO:240:

TGGGCTATGC	GCTTCGACGC	CGGTGCGCGG	TCAACGCGCC	GGAGGCAATC	GCTTCGCTGC	60
CGAGGAATGG	TTGCATCAGC	ATCGCACTGT	GCGGTCTGTG	ACCGACACCG	CGGTCCAAAGC	120
TGAAGTACGG	CGCGAAATAT	GCGCGAAATC	TCCGCTCTAG	TTCACTCTCG	GCGGCTAAAG	180
GTTCGGAAG	TTGGTTCGCG	GCTTCTGGGC	GAACGCGCGC	GCGGCTTCTT	TGGGCTCTCT	240
GGACAGGAAG	ACCTTGATCG	CGATCTGGGT	GTGCACTCTT	AACCGCTCTT	TTTCGGGCAT	300
GCACTCGCTC	TCCCGATATG	ACCGCAAGAT	GCGCTCTACG	GCGACGGGTC	CGTTAGCCGA	360
GATGCGCTCG	GCAAGTCTTA	GAACCTTGGT	CAACGCGCTG	CGTTCGGGCA	CACGTGCGCC	420
AT						422

## (2) INFORMATION FOR SEQ ID NO:241:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA

## (X1) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GCGTCCGCTT	GAACACGACG	CGCGCGCTGC	CAGATCTCCC	GGACTCGGTA	GTGCGCGCGG	60
TGGGCTCTGT	GCTCTCTTGA	CGCGCGCGCG	CGACCATAGG	GTGCTTAATG	CCGAGGTAGC	120
GCGCCAGGTG	CATGAGAGTG	ATGATGATGC	GACTCTCCAG	CTGCGCGACG	GGGAGCTTGG	180
CATCGCGGCT	GATCAGCCAG	GACCGGTAGG	ACAAGTGGAT	CGAATGCATA	GTGCGCTTCA	240
GAGTGGCGGT	CGCACTTCCG	GCTGCTTCCA	CGGCAATGCG	CTTGATTCTT	AGCTCCGCGT	300
AGTGTTCGCG	CATCGCGCTG	GCGATGAATG	GGACCGCGAG	GATGCGGACA	AACGGGCTCT	360
ACCTCAGGTT	TGCGGCTTGG	CGCACAGTGG	TGACAGCTCG	GTACTCGGCA	TAATGCTCTG	420
CGCCGA						426

## (2) INFORMATION FOR SEQ ID NO:242:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

AGACCCGCCA	GGGTGTGTC	GCTGCCCGCG	GCTTTGTGCA	TAATCTGCCG	TGGGTCCAGC	50
CGCCGATCAA	CTAGTGAGGC	GGAACGCTAG	GCTTTGGGAT	ACCCACGCTT	AAAAAGTTTA	100
TCAAAGAAAC	GAAGAAGGTT	GCCATGAGCA	CTGTTCGGCG	CTACCCCGCC	ATGTCCGCGA	150
CGGAACCGCT	GACCAAGACC	ACGATCACCC	GTCCGACCC	GGGCCCCGAC	GACATGCGCA	200
TGGACATCAA	ATTCCCGGGA	ATCTGTGCT	CGGACATCCA	TACCGTCCAA	ACCGAATGGG	250
GGCAACCGAA	TTTACCTGTG	GTCCCTG				300
						327

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Asp	His	Gly	Gly	Pro	Ala	Thr	Asn	Pro	Gly	Ser	Gly	Ser	Arg	Gly	Gly	1	5	10	15
Ala	Gly	Gly	Ser	Gly	Gly	Asn	Gly	Gly	Ala	Gly	Gly	Asn	Ala	Thr	Gly	20	25	30	35
Ser	Gly	Gly	Lys	Gly	Gly	Ala	Gly	Gly	Asn	Gly	Gly	Asp	Gly	Ser	Phe	40	45	50	55
Gly	Ala	Thr	Ser	Gly	Pro	Ala	Ser	Ile	Gly	Val	Thr	Gly	Ala	Pro	Gly	60	65	70	75
Gly	Asn	Gly	Gly	Lys	Gly	Ala	Gly	Gly	Ser	Asn	Pro	Asn	Gly	Ser		80	85	90	95
Gly	Gly	Asp	Gly	Gly	Lys	Gly	Gly	Asn	Gly	Gly	Ala	Gly	Gly	Asn	Gly	100	105	110	115
Gly	Ser	Ile	Gly	Ala	Asn	Ser	Gly	Ile	Val	Gly	Gly	Ser	Gly	Gly	Ala	120	125	130	135

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

```

Met Ala Ala Ala Gly Thr Thr Ala Asn Val Glu Arg Phe Pro Asn Pro
 1           5           10           15
Asn Asp Pro Leu His Leu Ala Ser Ile Asp Phe Ser Pro Ala Asp Phe
 20           25           30
Val Thr Glu Gly His Arg Leu Arg Ala Asp Ala Ile Leu Leu Arg Arg
 35           40           45
Thr Asp Arg Leu Pro Phe Ala Glu Pro Pro Asp Trp Asp Leu Val Glu
 50           55           60
Ser Gln Leu Arg Thr Thr Val Thr Ala Asp Thr Val Arg Ile Asp Val
 65           70           75           80
Ile Ala Asp Asp Met Arg Pro Glu Leu Ala Ala Ala Ser Lys Leu Thr
 85           90           95
Glu Ser Leu Arg Leu Tyr Asp Ser
100

```

## (2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```

Ala Tyr Ala Leu Arg Ser Arg Cys Arg Val Asn Ala Pro Glu Ala Ile
 1           5           10           15
Ala Ser Leu Pro Arg Asn Gly Ser Ile Thr Ile Ala Val Cys Arg Arg
 20           25           30
Ala Pro Thr Pro Pro Ser Asn Val Asn
 35           40

```

## (2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```

Val Pro Leu Asn Thr Ser Pro Arg Leu Pro Asp Leu Pro Asp Ser Val
 1           5           10           15
Val Pro Pro Val Ala Ser Leu Leu Ser
 20           25

```

## (2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```
Met Ser Thr Val Ala Ala Tyr Ala Ala Met Ser Ala Thr Glu Pro Leu
  1           5           10           15
Thr Lys Thr Thr Ile Thr Arg Arg Asp Pro Gly Pro His Asp Met Ala
  20           25           30
Ile Asp Ile Lys Phe Ala Gly Ile Cys Arg Ser Asp Ile His Thr Val
  35           40           45
Gln Thr Glu Trp Gly Gln Pro Asn Leu Pro Val Val Pro
  50           55           60
```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```
GCTTGGAGCC CTGGAGCCAC GGTGTGGTTC TGGGGGTGGA TTCTTTCTCG GCGAAGTCA 60
ACTAAGAGCC ACCTTGACAC CCAACCGGCG GCCCGGCTG GCGGTGCGG GCTAGAAAG 120
TTTGACCGCG GCGCGAAGCG TTCTGTGCTG CGGCGCATGC AGATGCGACA GCGTTGCTTG 180
AATCATCGGT GGAGCTCGGT GTAACTCCAG GCT 213
```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```
CCGAGTGTCT GTTCGCGCCC GCGGTGCGG GCGGCGCGCG TGGGCGCGGC ACCGACGGCG 60
GGCGCGGTGC TACCGCGCGG ACCGCGCGAC ACGGCGGAGT GCGCGCGGAC GCGGATGGC 120
TGGCACCGCG CGGCGCGCGG GGGGCGCGCG GCGAAGCGCG GCGAGGTGGT GCGCGCAGCG 180
ATGCTGCGCG GTTGGGTGCT ACCGCGCGGA CGGGCGGTAC GCGCGCGCGC GGTGCGCGCG 240
GCGGTGCGCG CACTGTGCTG CTGCGCGCTG GCGGACAGCG GCGGCTCGCG GCGCGCGCGG 300
GACAGGCGCG CACCGCGCGG GCGCGCGGGA GATGGCGTTC TGGGCGGTGT CAGTGCGACT 360
GGTGGTA 367
```

## (2) INFORMATION FOR SEQ ID NO:250:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA

## (X1: SEQUENCE DESCRIPTION: SEQ ID NO:150:

AAGCGCTGAT	TGGCAAGAG	ACCGCGCAGC	GGCGCGTAGC	CGCGGGACGG	CCGAGCGCGC	60
GACGCGACG	CGCGTGTGCT	GACCGCGGTA	CGCGGACCGG	TGCGGTGACG	TGCGGTGCGT	120
CTACTTGCAC	GCCAGCGCGT	TGCTCAAACT	TGTCACCGC	GAGACGAGGA	TGCGGTGCGT	180
GTCGCGCTGT	TGGACGCGCT	CGCGACGCGC	ATTGTCGAC	CGCGTGCGCT	ACCGCGAAGT	240
CGCGCGCGTA	CTCGTGTGAA	CGCGCGCGCA	TGTCACGCTA	ACCGGATCGG	ACCGCGCGGA	300
CGCGACGCGT	GACTGGGAGC	AGCTTGGGCG	ACCGCGCGCC	TGCGTGAAGT	GACGCGCGCG	360
GTTGAAACGC	AGTCGCGGCA	GTCGCGCGGA	ACGACATGCT	TACGCGGGAC	CGACACCGTT	420

(2) INFORMATION FOR SEQ ID NO:251:

## SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 399 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## 121 MOLECULE TYPE: CONA

## (84) SEQUENCE DESCRIPTION: SEQ ID NO: 264

CTTCTTCTTGGG	TGGCATGCGG	GGTACGGGCG	GAACCGGCGG	CAACCGCGGT	ATGGTTCGCG	60
CGCCGCGCGG	GCGCGCGCGT	GCGCGCGCGT	TGACGTTTAC	CACGCGCGGT	GCGGCTTGGG	120
GCGCGCGCGG	GCGCGCGTGG	CTGTTCACCA	GCGCGCGGT	GCGCGCGCGC	GGTGGGACCG	180
GTTCACACGG	GCGCGCGCGC	GCGCGCGCGG	GCGCGCGCGG	TTTGTTTTGT	GCGGGCGCGA	240
TGGCGCGGCG	GCGCGCGATT	GCGGATACCA	GAACGCTTGG	CTTCTTCTTGG		300

## (2) INFORMATION FOR SEC ID NO. 252.

## (1) SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (11) MOLECULE TYPE: protein

## (1X) SEQUENCE DESCRIPTION: SEQ ID NO: 132

Leu Glu Pro Trp Ser Asp Gly Val Gly Leu Gly Val Asp Ser Phe Ser  
1 5 10 15  
Ala Lys Val Asn  
20

## (2) INFORMATION FOR SEQ ID NO:253:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: protein

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```

Glu Leu Leu Phe Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly
 1           5           10           15
Thr Asp Gly Gly Pro Gly Ala Thr Gly Gly Thr Gly Gly His Gly Gly
 20           25           30
Val Gly Gly Asp Gly Gly Trp Leu Ala Pro Gly Gly Ala Gly Gly Ala
 35           40           45
Gly Gly Gln Gly Gly Ala Gly Gly Ala Arg Ser Asp Gly Gly Ala Leu
 50           55           60
Gly Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly
 65           70           75           80
Gly Arg Gly Thr Leu Leu Leu Gly Ala Gly Gly Gln Gly Gly Leu Gly
 85           90           95
Gly Ala Gly Gly Gln Gly Gly Thr Gly Gly Arg Arg Arg Trp Arg
100           105           110
Ser Gly Gly Cys Gln Trp His Trp Trp
115           120

```

## (2) INFORMATION FOR SEQ ID NO:254:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: protein

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

Gly Val Ile Gly Lys Ala Thr Ala Gln Arg Pro Val Ala Ala Gly Arg
 1           5           10           15
Pro Arg Pro Arg Pro Gln Arg Pro Val Ser Asp Arg Val Ser Asp Gln
 20           25           30
Arg Arg

```

## (2) INFORMATION FOR SEQ ID NO:255:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```

Leu Val Gly Gly Ile Gly Gly Thr Gly Gly Thr Gly Gly Asn Ala Gly
 1           5           10           15
Met Leu Ala Gly Ala Ala Gly Ala Gly Gly Ala Gly Phe Ser Phe
 20           25           30
Ser Thr Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Leu Phe
 35           40           45
Thr Thr Gly Gly Val Gly Gly Ala Gly Gly Gln Gly His Thr Gly Gly
 50           55           60
Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe Gly Ala Gly Gly Met
 65           70           75           80
Gly Gly Ala Gly Gly Phe Gly Asp His Gly Thr Leu Gly Thr Gly Gly
 85           90           95
Ala Gly Gly

```

(2) INFORMATION FOR SEQ ID NO:255:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```

TCCTGTTCCG CGCCGGCGGG GGGGCGGGTG TTGGCGGTGA CGGTSTGGCA TTCTGGGCA 50
CGGCCCCCGG CGGGCCCCGT GGTGCCGGCG GGGCGGCTGG GCTTTTCAGC STCGGTGGGG 120
CGCGCGCGCG CGCGCGGAAT CGATTGGTGG GGAACACGCG TCCCGGGGGG TCCGCGGGT 180
CGGCGCTGCT CTGGGGCGAC GGGCGTGCCG GCGCGCGCGG TGGGGTCGGG TCGACTACG 240
CGGCTGCGCG CGGGCGGGCG GGCAACGCCA GCGTGTCTGT AA 282

```

(2) INFORMATION FOR SEQ ID NO:257:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```

CGGCGACGAG CGTGCTACTG GTCAACTGAT GCGCTGATG TGACCTTCCG GCGCGCGGAT 60
CAGTGCTTCT CAGGACCGAC GTAATATTGG AAAACCAATC CGGCGCGCGA GCGGAGGATG 120
AATGCCACAC CGCGCGCGAT CAGCCACGCG AGCCACAAGG CGATGCGGAC CGCTGCCACC 180
GAGCGCGACA CGCGACCAT GATCGGCCAC CAGCTATGCG GACTGAAGAA TCGAGTTCT 240
CGTGCGCGCT CCGTGATTTC AGCGCTTGG TAGTCTCTCG GCGCGGAATC TAACCGCGCG 300
GCCACAACCG GGAAGAGGTT GCGGACGATC AACCGCATGC CCGCGGTGAG CGCCACGCGA 360

```

ATGGTGGCAG CCCATCTGAC ACCACGGGTG GCGAACATCG AGGTCAACAC GCGCT

415

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

TCACCGCGTG AACGTTTCCT AACACTGATA CGTATGCTTG TCAGCCBAGCA GATCAAGTCC	60
AGTCCBAGCA ATGCCAGGAG ATCATCGGCT AGGCTCACGG TTTCGCTGG GACBAGAGCG	120
TATCGAGTTC TGCGCTTGA GGTGCGGTGG CTTGCTGGGA AGTCTGACGC GGCATCAGAA	180
CGGTTGTCAA TACCGTCTT TGGGGGATAT GGCCTATTTT CTCTCTCGG GCGCTCCAC	240
CGGATCTGTT TTGGAAGCTT GCGCAAGCGC GGTCCAGTTA CGGCTCTTTC ACTCGCGCT	300
GCGGTAGCTG CGCGGCTCG ATCGGTTTGA ACCTCATGCG AATTCGCGCA ATGGGTGAGT	360
ACCTGACGCT CTT	373

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

CCAAACGGGA CAGGCGCGCC GCGACGGTGG GAAGTTGCAC CAGCGTGCCG GCTCATGTA	60
GCCTACCGGT GAGCACGGCG TAGACAGCAG ATCCGTGGAT CCGCGCTTCC GTGTGCTCCG	120
CGCCGAGTAC CGCGCGCGCG AACCTCAGCG ACCAAGGCAA CGCGATCGAT ACCGGGATCG	180
CGACTCTGTC CGAATTCGAG CTCTCTCGAC AAGCTTGCGG CGGCACTGCA ACCCGGCTGA	240
ATGATTGAGT TTAAACCGCT TAGCAATAC TAGCATAACC CTTTGGGGCC TCTAAACGGG	300
CTTTGAGGCG TTTTTCCTG AAGGAGGAAA CTATATCGGG ATAACTGCG CTACTAGCGA	360
AGAGGGCGGC ACUGATCGCC CTCTCCAACA GTTGGCGCAG CTGAATGCGG AATGACCGCG	420
CCC	423

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:



AGTGGCCAGC	CGGTGGGCGA	ATGCATCCAG	CTCCGGGTAC	GTGAGCTGAC	CATCGGCGCA	60
ACTGACCGCC	ACCGAGTCAG	GCTGTGCGCC	AGCGATTTCG	GCGAACCGGG	TATGCACCGG	120
GGGTGCCGAC	GTGTGCACAT	CGGGCAGGCG	GGGTGCGGTC	GGATCGTGCT	CGCCGTCCAG	180
CAGAATGTGG	AGTGTGGCGA	CGCGGGGATC	CCACCGGGTG	ACCAAGCGCT	GTAAACACAGC	240
CAGCAGCTGG	CTGGCGAGGC	TTTCGGGCGC	CATGGTGGCC	AGCGCACCGT	CGAGCACCTG	300
CATTAGCAGC	GTGAGCTCAC	CGGTGCTAGG	GTGGCGGGCG	ACGGTCACCG	GAAGTGCGA	360
CAAACCTCTT	AGCGCCACCG	GACGGAAAGT	CACCGCGTTT	GGGA		401

## (2) INFORMATION FOR SEQ ID NO:261:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA

## (12) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GTCTGTGTCG	CAGGCTGTTT	TTGGAACCGG	CTGGCTAACT	TGGCACCGGG	GTATCCCGCC	60
ACGATCGAAG	CGGCCCAACC	CGCGGTGTCA	CGGCTACTT	CGCAAGACCG	GGCGGTGCA	120
GTGGGACGAC	TGAGCGGCGA	CGCGGGGGGG	CGACTATTGG	ACACCGGCAC	CGCGCAATTG	180
GTGGCTCTGC	CGCGGGGGGG	CGATTCTGGG	CGACCGGCGA	GCATCATGGT	CTTGATGAC	240
ATGGACCTTG	CACCGCGCGT	CATTCTTCTG	CGGGCGCGGG	CAGCGCGGTT	GACGAGCGAC	300
GACGACGCGA	CGCGCTTCTT	TGCGGCGCGG	CGCGGCTACT	TCTTGGCGGA	CTGTCTCTTC	360
GTGCACACCG	CAGGATGGA	TGTCCTGTAC	CGAGCGGACA	CGGATTTCAC	CGCGATCGCC	420
C						421

## (2) INFORMATION FOR SEQ ID NO:262:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: Linear

## (11) MOLECULE TYPE: cDNA

## (12) SEQUENCE DESCRIPTION: SEQ ID NO:262:

ATGATATATCA	CGCTCAACGC	CATCTTGGGT	GGGATCTTCC	GGCGCGCGCG	CAGTGAACCTA	60
GACGAGCTGC	CGCGGCTCAT	TGCGCGGTGG	GTGACGCTGG	GCTGCGGCTT	GGCGGCGCTA	120
CGGAAACCGCA	AACCGGACTA	TGGCGCGCTT	AGCGCGTGGG	CGCGGCTGGC	CGAGTGGCGG	180
CGCGAGTACG	ACACTGTGAT	CGACGAGCTC	ATCGAAGCGG	AGCGGGGCGA	CGCGAACTTC	240
CGCGATCGGA	CGGACGTTTT	GGGTTTCATG	CTGGCGAGCA	CTTACGACGA	CGGTTCCATC	300
ATGTGCGGCA	AGGACATTGG	CGAGGAAAGT	CTCACGCTGC	TTGCGCGCGG	CGACGAAACT	360
ACGCGCGCGA	CATGGGCTGG	GGTTTGAAG	GGCTCAACCG	GCACCGCGAC	GTGCTGGCGG	420
CTCTGG						426

## (2) INFORMATION FOR SEQ ID NO:263:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GTCTGGTGG	CAGGCTGTTG	TTCGAACCCG	CTGGCTAACT	TGGCAGCCGG	GTATCCGCCG	60
AGCATGGAC	CCGCCGAAC	GGCCGTGTCA	CGGCTACTT	GGCAAGACCC	GGCCGGTGCA	120
GTGGCAGAC	TGAGCGGCA	CCGCCGGCG	GCATTAATCG	ACAAGCGCAC	CCGCCAATTG	180
GTGGCTGTC	CCGCCGGCG	GGATTGGCG	GCACCGGCCA	GCATCATGGT	CTTCGATGAC	240
GTGCAGTTG	CAGCCGCGT	GATTTTCTG	CCGCCGGCG	CAGCCGCGT	GACCAAGCAC	300
GACCAAGCA	CGGCTTCTT	TGCCGCCCG	GGCGGCTACT	TGGTGGCGCA	CCTGTCTCTC	360
GTGCACACG	CAGGAGTGA	TGTGCTGAC	GCAGGCGACA	CGGATTTCAC	CGCGATCGCG	420
CGCGGTCCG	ACGCGAAGT	GGTCTGGGC	AGCGCAGATG	GGCGGTCTA	CAGGTTGGC	480
AAGAACCGC	AGTTACCTG	CGTGGCGCG	CC			522

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 739 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GTCTGGGCGC	ACGCGGTCC	GGCGGCTTCA	GGCGGTGGCG	CGAGAGCCCG	CGCAAAACCA	60
ACCGTGGCGC	TTAGTGGCT	GGCGGCGCG	CGGTGTGCT	GTCTCTGGT	TTGGGCGCCA	120
TGGCATCTG	GATCGGATC	GGCGGAGGC	CGGTACAGCC	GGTTCAGCG	GTTCGGGAGG	180
AGCGCTTAG	CGCGTACTG	TGGAAGTCT	CAGAACTCA	CGCGGTGATG	GGCTGTCTGT	240
GCATCGACG	GGCGAAGCG	ATGACATCG	TGGACTCTT	CGCGGTGACG	GTGTCTCTGC	300
CGGACTGCG	GGGTGCGTG	TATACGAGC	AGGATCGGT	GTATGCGCG	ACCGCTTACA	360
CGCGCATCA	CGCGTATTT	TGATCGGAGC	CGCGGCGACA	GTACGAACAT	TGGGTGAACG	420
AAGCGTCTG	CGCGTTTTCG	ACCGGCGACA	AAGCGCGCG	GTCTGTGCG	ACTTGGCGCG	480
ACAATGGA	GAACTGCGCA	GGCAAGACCG	TGACGCTCAC	GAATAAGCG	AAGACCTTACC	540
GGTGGAGCT	TGGCGAATTC	AAAGGAGCT	CGCGGAGAT	CAGCGGTGTA	GACACCCAA	600
AAGCGCTGA	GGGTGGGAA	TGGCAACCG	CGATGAGCT	GGCCAACAT	GTGGTTTCTG	660
ACGTCAACG	ATGCGGATAC	CAGATACCA	ATCAAGCAG	CGAGATCGCC	GGCAGATCT	720
GTTCACAAAG	TGACACAG					739

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

AGACGTCGTC GAGGCGGCCA TCGCCCGCGC CGAAGCCGTT AACCCGCGAC TGAACGCGTT 60  
GCGGTATGC 69

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

ACTGCACCGG	GCAGCGCCGA	CCAACGGATC	GGGTCAACTA	GCAGTCCCGG	TGGAGGCGCC	60
CCCGCGGTC	GTGCGTTCCG	ACGCGGGAAC	CTTGGGCGAG	CGCGCTCCAG	AAGGTTGGA	120
GGGAGAGTTC	GACGACGCTA	TGCACGAGCG	GTTCGCGGTC	TTGAGCTCCG	CGAGTCTGGC	180
CGAAGCGCTG	CGCGGTCGCG	TGACCCCGAT	GACGCTGGAT	GTCCAGTTGA	GTGACTCGCG	240
CCCGCGCGGT	CGCGCGATGG	GTTCGGTACT	GGCGCTTGGC	GGTGTCTGTT	CGGATGAGTG	300
CGACAGAGAA	GCGATCGCGG	TGTTGGGTCA	CCGCGCGTAT	ATCGGAGTGT	CGGCCAATAT	360
TGTGGCGCGC	GCGCAACTCG	CGCGGTGGGA	CGCGCAGCGC	GTAACCCGCG	GGGCACTGGG	420
CGAGCAACCG	CAGGTCACTG	AGCTGCTTCC	GTTCGCTCGA	CGGCAACTTG	CGGCGCGACC	480
GCTCGCGCTG	GTTCGGAAGG	TGGTCTGAC	GCGACGCTCG	CTG		523

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GTGTCGGTGT	GTTCGGGCTA	GCAGCGACTT	CCCGCGCGCG	CGCGCGCGCG	GGAGCGGGCT	60
CTGCAGAGAC	CGGTGCGCGC	GCGCGCGCGC	GGGCGACCAA	AGCGCGGATC	GATTCGCGCA	120
GCGGCTTGGC	CGCGCGCTTG	TCCACTCGGT	TGTTGGCGGT	CCCGAGCCAT	ACCCAGAAAC	180
AACGCTGAAG	GCGCGCGCGC	TCCGCTCGGT	TCCCGCGCGG	CGAC		224

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

TGAAGTACT	GCGCGCGCTG	ATCGCGCGCG	GCGCGCTGTC	ATAGGTGCGC	CGCCAGGCCA	60
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TGAAGTGGTC	TTGGCCATAG	CGGGGCTTGG	TCTGGGCTTT	GTCCAAACCC	TGCAGCGGCG	120
CGTAGTGGCG	TTGGTTGAGC	CGCCAGGTAC	GGCGGACGGG	AATCCAGAGC	CGATCGGCGC	180
TGTCCAAAGC	CAGATGCGCG	GTGGTGATCG	GGCGGCGCAG	CAACGAGGTG	TAGAGCCAGT	240
CGGGCAATAG	GTGGTGTTCC	CGGATCAGCT	CGCGGCTTGG	AACGGGCTCT	GGTTGGGCGT	300
TGTGGTTGAG	GGCGACATCG	ACCCAGCGGG	TGAACAGGTT	GAGGGCATTC	CAGTCGCTCT	360
CGCGGTTGGG	CAGCAACAGC	AGGCTGCGAG	TGTTTGCCAT	ACCGGCAAGT	CTCTCAGCGA	420
CTCGCGCACT	CTGTATGGTG	GACCAAAATG	CCCGAATCTT	CGTCGGTCCG	CTGGCCAGCG	480
CGTTCATACC	GGCGAGGTGG	TGGGACCGGT	AACGGCGGGT	T		521

## (2) INFORMATION FOR SEQ ID NO:269:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

CTCCAGGCTC	ATTGCGTGA	ACAAAGCCAC	CGGCGGTAC	AGCGGACGCC	CGCATTCGTT	60
GTCTGTGATG	TGGCGGTACA	GTGGGCGATC	GGGCGCTGGA	CGAAGCTCCG	CGCAGGGGCA	120
GGGAAGCAGC	CGGTGCGGCG	TGACGCGGGG	TGAGAACGCT	AGTGCCAGAC	AGTCTCGCGG	180
CGCGAAGGTC	TTGACGGGTC	AGACTGGGCC	TGGCGCTCTT	CGGACGAGCG	GTGATCGGCG	240
CGGAGCTGAG	AGGCTAGGCT	CTCGAGCTCA	CGGCGGAGCC	GTTCAGGACC	CGAGTCCACC	300
TGCGTGGTCT	TGTTGCGGCG	CAGCACCTGG	GTGAAGTTGA	CGCGCTCGAC	ATCGGCGCGG	360
GTGAGCCGGA	ACGCGCGGAC	CGTGGTGGCC	GTGGTGGGCC	GGGCGAGGGG	CGGCAACTGC	420
TGCGCA						426

## (2) INFORMATION FOR SEQ ID NO:270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

CGGAGACGGG	CGGACAAAGC	GCAATCGGCT	TGGCGCGGCG	CGCGCGCGCG	GACCGGGGCT	60
AGGGCGGGCG	CGGCGCGGGA	CTGTGGGGTA	CTGCGGCGCG	CGCGGAGCAC	CGCGGGGCAA	120
GGCGGTGGTA	CGGCGGGGCG	ACCGTTGGCC	GTTCAGGCGAG	GCATGGGCGC	CGCGGTGGCG	180
GGCGGTGGCG	TGATCGGCAA	CGGCGGGGCG	GGCGGCGGAC			219

## (2) INFORMATION FOR SEQ ID NO:271:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```

AAGATCATCG GCGCGCTGCG TTAGCATCGC TCGCTCTGCG ATCGTCGCGG GCGCGGATCA      60
CGGAGGTCCG GCCTTGTACC CCACTGCTCG AACGTCGAGC ACCACATCGG GGTCTCTGGG      120
ATCCTTTTCG ACCTTGGCGG GCAGACGCTG GACATGCACG TTCACCAAGC TGTATCTGGC      180
TGGTGCCTGG TAACCCGATA CTTGTTCGAG CAGACATCA CGAGTAAACA CCTGCGCGCG      240
CTTGCGCGCC AATGCGACCA ACAGGTGGA TCCAGCGGT GTGACGAGA TGTGCTCACC      300
GTTGCGAGTG ACCTTGTGCG CCGGTACGTC GATTTCTACG TGGCGATGG ACAGCATCTC      360
GCGCGGTTCC TCGTGTTCG GCGCGAGCGG CCGCGCGACC CCGGCAACCA GTCCTTGGG      420
CTTGAACGGC TTCATGATGT AGTCGTGCGG CCGCGACTCG AGACCCAGCA CCACATCCAC      480
GGTGTGCGTC TTGCGGTGA GCATCAGCAT CGGAACCGG GATCTGGCGG GCAACACCGG      540
GCACACGCTG ATGCGGTTCA TACCGGGGCA A                                     571

```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```

Leu Phe Gly Ala Gly Gly Val Gly Gly Val Gly Gly Asp Gly Val Ala      1
1      5      10      15
Phe Leu Gly Thr Ala Pro Gly Gly Pro Gly Gly Ala Gly Gly Ala Gly      20
20      25      30
Gly Leu Phe Ser Val Gly Gly Ala Gly Gly Ala Gly Gly Ile Gly Leu      35
35      40      45
Val Gly Asn Ser Gly Ala Gly Gly Ser Gly Gly Ser Ala Leu Leu Trp      50
50      55      60
Gly Asp Gly Gly Ala Gly Gly Ala Gly Gly Val Gly Ser Thr Thr Gly      65
65      70      75      80
Gly Ala Gly Gly Ala Gly Gly Asn Ala Ser Leu Leu Val                  85
85      90

```

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```

Met Pro Pro Val Ser Ala Asn Ala Met Val Pro Ala His Ser Thr Pro      1
1      5      10      15
Pro Val Ala Asn Ile Glu Val Asn Thr Pro

```

20

25

## (2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Lys	Pro	Asp	Arg	Pro	Ala	Ala	Thr	Val	Gly	Ser	Cys	Thr	Thr	Val	Arg
1					5				10					15	
Ala	Pro	Cys	Ser	Gln	Pro	Val	Thr	Thr	Ala						
			20						25						

## (2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Trp	Pro	Ala	Gly	Arg	Pro	Met	His	Pro	Ala	Pro	Gly	Thr	Ser	Ala	Asp
1					5				10					15	
His	Pro	Pro	Asn												
			20												

## (2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Val	Leu	Val	Ala	Gly	Cys	Ser	Ser	Asn	Pro	Leu	Ala	Asn	Phe	Ala	Pro
1					5				10					15	
Gly	Tyr	Pro	Pro	Thr	Ile	Glu	Pro	Ala	Gln	Pro	Ala	Val	Ser	Pro	Pro
			20				25					30			
Thr	Ser	Gln	Asp	Pro	Ala	Gly	Ala	Val	Arg	Pro	Leu	Ser	Gly	His	Pro
	35					40					45				
Arg	Ala	Ala	Leu	Phe	Asp	Asn	Gly	Thr	Arg	Gln	Leu	Val	Ala	Leu	Arg